

95247

STIC-Biotech/ChemLib

From: Chan, Christina  
Sent: Wednesday, May 28, 2003 5:23 PM  
To: Chen, Shin-Lin; STIC-Biotech/ChemLib  
Subject: RE: sequence search: 09/865,018

**Please rush. Thanks Chris**

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
308-3973  
CM-1, 9B19

-----Original Message-----

From: **Chen, Shin-Lin**  
Sent: Wednesday, May 28, 2003 5:18 PM  
To: Chan, Christina  
Subject: sequence search: 09/865,018

I need case to work on for next bi-week. Please approve the following **Rush sequence search for 09/865,018**. Thanks!

**SEQ ID Nos. 2, 4 and 6.  
amino acid residues 22-88 of SEQ ID Nos. 2, 4 and 6.**

Shin-Lin Chen  
AU 1632  
CM1 12A15  
Mail Box: CM1 12E12  
(703) 305-1678

Searcher: Fl. Smith  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 5/30/03  
Date Completed: 6/3/03  
Searcher Prep/Review: 7  
Clerical: \_\_\_\_\_  
Online time: 10

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: 6  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_





# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number:** 97-03-1212

**TO: Shin-Lin Chen**  
**Location: cm1/12e12/12a15**  
**Art Unit: 1632**  
**Tuesday, June 03, 2003**

**Case Serial Number: 865018**

**From: Mona Smith**  
**Location: Biotech-Chem Library**  
**CM1-6A01**  
**Phone: 308-3278**

**mona.smith@uspto.gov**

### **Search Notes**







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Query Match
Best Local Similarity 100.0% Score 484 Length 199
Matches 67 Conservative 0 Mismatches 0 Gaps 0

1 1 EHPKOSAGTPEPWVHEETWETKRGHMEFASQPKWNI FQNRKHEGKYEWQFVER 60
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45 61 GSLEFF 67
1 1
14 72 GSLEFF 88

RESULT 4
US 09 902 572 24
Sequence 24 Application US/09090901
Patent No. US2002008706A1
GENERAL INFORMATION:
APPLICANT: Nanda Lal, Krishna
APPLICANT: Yash, Mehta
TITLE OF INVENTION: P27(KIP-1) PRK112 Protein Complexes
FILE REFERENCE: Ciba-14 CON (1966 514 CON)
CURRENT APPLICATION NUMBER: US/09/970,561
CURRENT FILING DATE: 2001-10-04
PRE-K APPLICATION NUMBER: P1/98/971,659
PRE-K FILING DATE: 1999-09-18
PRE-K APPLICATION NUMBER: BRN 09/119,765
PRE-K FILING DATE: 2000-12-14
NUMBER OF SEQ. TO NO. 6
SOFTWARE: Patent In Ver. 2.1
SEQ. ID NO. 2
LENGTH: 199
TYPE: 191
ORIGIN: Homo sapiens
US 9 902 572 24

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Query Match
Best Local Similarity 100.0% Score 484 Length 199
Matches 67 Conservative 0 Mismatches 0 Gaps 0

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14 22 EHPKOSAGTPEPWVHEETWETKRGHMEFASQPKWNI FQNRKHEGKYEWQFVER 60
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45 61 GSLEFF 67
1 1
14 72 GSLEFF 88

RESULT 4
US 09 902 572 24
Sequence 24 Application US/09090901
Patent No. US2002008706A1
GENERAL INFORMATION:
APPLICANT: Nanda Lal, Krishna
APPLICANT: Yash, Mehta
TITLE OF INVENTION: P27(KIP-1) PRK112 Protein Complexes
FILE REFERENCE: Ciba-14 CON (1966 514 CON)
CURRENT APPLICATION NUMBER: US/09/970,561
CURRENT FILING DATE: 2001-10-04
PRE-K APPLICATION NUMBER: P1/98/971,659
PRE-K FILING DATE: 1999-09-18
PRE-K APPLICATION NUMBER: BRN 09/119,765
PRE-K FILING DATE: 2000-12-14
NUMBER OF SEQ. TO NO. 6
SOFTWARE: Patent In Ver. 2.1
SEQ. ID NO. 2
LENGTH: 199
TYPE: 191
ORIGIN: Homo sapiens
US 9 902 572 24

```

```

Query Match
Best Local Similarity 100.0% Score 484 Length 199
Matches 67 Conservative 0 Mismatches 0 Gaps 0

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1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
14 22 EHPKOSAGTPEPWVHEETWETKRGHMEFASQPKWNI FQNRKHEGKYEWQFVER 60
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45 61 GSLEFF 67
1 1
14 72 GSLEFF 88

RESULT 4
US 09 902 572 24
Sequence 24 Application US/09090901
Patent No. US2002008706A1
GENERAL INFORMATION:
APPLICANT: Nanda Lal, Krishna
APPLICANT: Yash, Mehta
TITLE OF INVENTION: P27(KIP-1) PRK112 Protein Complexes
FILE REFERENCE: Ciba-14 CON (1966 514 CON)
CURRENT APPLICATION NUMBER: US/09/970,561
CURRENT FILING DATE: 2001-10-04
PRE-K APPLICATION NUMBER: P1/98/971,659
PRE-K FILING DATE: 1999-09-18
PRE-K APPLICATION NUMBER: BRN 09/119,765
PRE-K FILING DATE: 2000-12-14
NUMBER OF SEQ. TO NO. 6
SOFTWARE: Patent In Ver. 2.1
SEQ. ID NO. 2
LENGTH: 199
TYPE: 191
ORIGIN: Homo sapiens
US 9 902 572 24

```

MOLECULE TYPE: Protein  
US-08-902-572-24

Query Match 100.0% Score 383; DB 8; Length 348;  
Best Local Similarity 100.0%; Pred. No. 2, 4e-37;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDONHKPLEGKYEWQVEVK 60  
|||||  
Db 22 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDONHKPLEGKYEWQVEVK 61  
|||||  
QY 61 GSLPEFY 67  
|||||  
Db 82 GSLPEFY 88

## RESULT 5

US-08-902-572-8  
Sequence 2, Application US/08902572

Patent No. US20020068706A1

GENERAL INFORMATION:

APPLICANT: Gyuris, Jen

APPLICANT: Lamphere, Lou

TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND

TITLE OF INVENTION: RELATED THERETO

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08-902-572

FILING DATE: 29-JUL-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV-069.03

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 365 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Protein

US-08-902-572-9

Query Match 100.0% Score 383; DB 8; Length 365;  
Best Local Similarity 100.0%; Pred. No. 2, 6e-37;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDONHKPLEGKYEWQVEVK 60  
|||||  
Db 189 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDONHKPLEGKYEWQVEVK 248  
|||||

QY 61 GSLPEFY 67  
|||||

Db 249 GSLPEFY 255

## RESULT 6

US-08-902-572-6

Sequence 2, Application US/08902572  
Patent No. US20020068706A1

GENERAL INFORMATION:

APPLICANT: Gyuris, Jen

APPLICANT: Lamphere, Lou

APPLICANT: Beach, David H.

TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND

TITLE OF INVENTION: RELATED THERETO

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,572

FILING DATE: 29-JUL-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV-069.03

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 380 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US 08 902 572-6

Query Match 100.0% Score 383; DB 8; Length 380;

Best Local Similarity 100.0%; Pred. No. 2, 7e-37;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDONHKPLEGKYEWQVEVK 60  
|||||

Db 294 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDONHKPLEGKYEWQVEVK 263  
|||||

QY 61 GSLPEFY 67  
|||||

Db 264 GSLPEFY 270

## RESULT 7

US-08-902-572-2

Sequence 2, Application US/08902572

Patent No. US20020068706A1

GENERAL INFORMATION:

APPLICANT: Gyuris, Jen

APPLICANT: Lamphere, Lou

APPLICANT: Beach, David H.

TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND

TITLE OF INVENTION: RELATED THERETO

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk



Db 22 DHPKPSACRNLFGPVDHEELTRDLKXHCRCMEASQRKNWDFQNHKPLKCKYEWQVEVK 81

QY 61 GSLPEFY 67  
|||||

Db 82 GSLPEFY 88

## RESULT 10

US-08-902-572-26  
; Sequence 26, Application US/08902572  
; Patent No. US20020068706A1  
; GENERAL INFORMATION:  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Lamphere, Lou  
; APPLICANT: Beach, David H.  
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND  
; TITLE OF INVENTION: RELATED THERETO  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US-08-902-572  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MIV-069 03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 237 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-902-572-26

Query Match 95.6%; Score 366; DB 8; Length 237;  
Best Local Similarity 95.5%; Prod. No. 1.6e-35;  
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
US-08-902-572-26  
; Sequence 26, Application US/08902572  
; Patent No. US20020068706A1  
; GENERAL INFORMATION:  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Lamphere, Lou  
; APPLICANT: Beach, David H.  
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND  
; TITLE OF INVENTION: RELATED THERETO  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,572  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 514

## RESULT 11

US-08-902-572-28  
; Sequence 28, Application US/08902572  
; Patent No. US20020068706A1  
; GENERAL INFORMATION:  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Lamphere, Lou  
; APPLICANT: Beach, David H.  
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND  
; TITLE OF INVENTION: RELATED THERETO

; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,572  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MIV-069 03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-902-572-28

Query Match 95.6%; Score 366; DB 8; Length 252;  
Best Local Similarity 95.4%; Prod. No. 1.7e-35;  
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
US-08-902-572-28  
; Sequence 28, Application US/08902572  
; Patent No. US20020068706A1  
; GENERAL INFORMATION:  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Lamphere, Lou  
; APPLICANT: Beach, David H.  
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND  
; TITLE OF INVENTION: RELATED THERETO  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,572  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 514

## RESULT 12

US-08-902-572-20  
; Sequence 20, Application US/08902572  
; Patent No. US20020068706A1  
; GENERAL INFORMATION:  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Lamphere, Lou  
; APPLICANT: Beach, David H.  
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND  
; TITLE OF INVENTION: RELATED THERETO  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,572  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 514

## RESULT 13

US-08-902-572-20  
; Sequence 20, Application US/08902572  
; Patent No. US20020068706A1  
; GENERAL INFORMATION:  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Lamphere, Lou  
; APPLICANT: Beach, David H.  
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND  
; TITLE OF INVENTION: RELATED THERETO  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,572  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 514



Query Match 39.9%; Score 153; DB 9; Length 164;  
 Best Local Similarity 44.3%; Pred. No. 1.5e-10;  
 Matches 27; Conservative 10; Mismatches 24; Indels 0; Gaps 0;  
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 Db 17 ACNLEGPVDSEQLSRDCLALMAGTQFAPERNNEDEVTTPLEGDFAWEPVPGLGLPKL 76  
 QY 67 Y 67  
 Db 77 Y 77

Search completed: May 30, 2003, 09:05:09  
 Job time : 6.8385 secs





Genforce version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003 09:52:12 : Search time 42.484 seconds  
(without alignments)  
604 476 Million cell updates/sec

Title: US-09-865-018b-2

Perfect score: 1064

Sequence: 1 MSNVRVNSGSESLERMARQ PNAISVFIEKKKILRPPEQT IQA

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 90476 seqs, 1325625 residues

Total number of hits satisfying chosen parameters: 90476

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database: A\_Genoseq\_101009.\*

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3: /SID52/gqdata/geneseq/geneseq-emb1/AA1942.DAT.*
4: /SID52/gqdata/geneseq/geneseq-emb1/AA1943.DAT.*
5: /SID52/gqdata/geneseq/geneseq-emb1/AA1944.DAT.*
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21: /SID52/gqdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gqdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gqdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1064	100.0	198	17	AAP92709 Human p27 Kipl. H
2	1064	100.0	198	19	AAW29717 27 kDa protein inh
3	1064	100.0	198	19	AAW46888 Amino acid sequenc
4	1064	100.0	198	20	AAI00768 CK1/KIP protein p2
5	1064	100.0	198	21	AAI97523 Human p27 protein
6	1064	100.0	198	21	AAI96052 Human cyclin depen
7	1064	100.0	198	21	AAI96066 Human cyclin depen
8	1064	100.0	198	21	AAI94400 Human p27(Kip1) ki
9	1064	100.0	198	22	AAI94449 Amino acid sequenc
10	1064	100.0	198	22	AAI48309 Human p27 protein.

#### ALIGNMENTS

```

RESULT 1
AAP92709
1: AAP92709 standard, Protein, 198 AA.
XX
XX AAP92709;
XX
XX 16-Jul-1996 (first entry)
XX
XX Human p27 Kipl.
XX
XX p27 protein; Kipl., cyclin E, Cdk2; cell proliferation; ulcer;
XX cancer, hyperplasia, diagnosis, therapy.
XX
XX Homo sapiens.
XX
XX W09602140-A1.
XX
XX 01-FEB-1996.
XX
XX 07-JUN-1995; 95W0-US07361.
XX
XX 15-JUL-1994; 94US-0275983.
XX
XX (HUTC.) HUTCHINSON CANCER RES CENT FRED.
XX (SLCK) SLOAN KETTERING INST CANCER RES.
XX
XX Koff A, Massague J, Polyak K, Roberts JM,
XX W09602140-A1.
XX 15557/11.
XX N-PSDB; AAT16336.
XX
XX p27, an inhibitor of cyclin E Cdk2 complex activation, and agents
XX which enhance and inhibit its activity, useful for treating
XX

```

```

11 1064 100.0 198 23 AAR47880 p27-Kip1 Homo sa
12 1061 99.7 198 21 AAY70307 Human mutant cycli
13 1064 99.4 198 20 AAW29717 Cdk inhibitor fusi
14 1064 99.4 198 20 AAW46888 Human p27-p16 fusi
15 1059 99.5 391 21 AAY97526 Human W3 protein s
16 1059 99.4 198 21 AAY96041 Antiproliferative
17 1059 99.4 198 21 AAY96066 Angiogenesis inh
18 1057 99.3 198 17 AAY79133 Human kipl. p27-ki
19 1054 99.1 365 18 AAW23536 CDK inhibitory fusi
20 1054 99.1 365 20 AAW95107 Human p16p27 fusi
21 1054 99.1 365 20 AAW95096 Human p16p27 fusi
22 1054 99.1 365 21 AAY97523 Human W3 protein s
23 1054 99.1 365 21 AAY96041 Antiproliferative
24 1054 99.1 365 21 AAY96071 Angiogenesis inh
25 1054 99.1 365 18 AAW23536 Cdk inhibitor fusi
26 1054 99.1 365 20 AAW95096 Human p16(GSp27 f
27 1054 99.1 365 21 AAY97523 Human W3 protein s
28 1054 99.1 365 21 AAY96041 Antiproliferative
29 1054 99.1 365 21 AAY96071 Angiogenesis inh
30 1047 98.4 365 21 AAY97527 Human W4 protein s
31 1047 98.4 365 21 AAY96042 Antiproliferative
32 1047 98.4 365 21 AAY96069 Angiogenesis inh
33 1044 98.1 194 20 AAW94930 Amino acid sequenc
34 976 91.7 198 23 AAW51589 Porcine p27Kip1 po
35 931 87.5 197 16 AAR79132 Murine kipl. p27-k
36 931 87.5 197 17 AAW92708 Mouse p27 Kipl. M
37 931 87.5 197 19 AAW29718 27 kDa protein inh
38 931 87.5 197 20 AAY08819 Mouse wild type p2
39 931 87.5 197 20 AAY08847 Murine wild type p
40 931 87.5 197 22 AAW46150 Amino acid sequenc
41 908 85.4 198 20 AAW95134 Human p27/p16
42 908 85.4 198 21 AAY97523 Human W3 protein s
43 908 85.4 198 21 AAY96041 Antiproliferative
44 908 85.3 334 21 AAY96071 Angiogenesis inh
45 905.5 85.2 348 20 AAW95104 Truncated p27/p16

```



```
XX PS Disclosure; Columns 17-18, 14pp, English.
XX CC
XX CC The present sequence represents a p27KIP1 protein, which is part of a
XX CC family of small cyclin-dependent kinase inhibitors. The proliferative
XX CC state of a cell transformed with human papillomavirus (HPV) can be
XX CC evaluated in the following manner: Cyclin/cyclin-dependent kinase
XX CC complexes containing protein p27KIP1 are isolated from the transformed
XX CC cell, and the HPV E7 oncoprotein (AAW46886) added to the isolated
XX CC protein. Cyclin/cyclin-dependent kinase complexes are isolated from an
XX CC untransformed cell that is substantially homogenic with the transformed
XX CC cell, and the HPV E7 oncoprotein added. The kinase activities of the 2
XX CC samples are measured, where a proliferating transformed cell has a
XX CC greater kinase activity than the untransformed cell. The method is
XX CC used for determining the extent of interaction and/or inactivation
XX CC between a cyclin/cyclin-dependent kinase inhibitor and the HPV E7
XX CC oncoprotein and thus evaluating the proliferative state of a transformed
XX CC cell.
XX CC
XX CC Sequence 198 AA:
XX CC
XX CC Query Match 100.0%; Score 1064; DB 12; Length 198;
XX CC Best Local Similarity 100.0%; Pred. No. 7 2e-100;
XX CC Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 1 MSNVVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRCRMEASQKWK 60
XX CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX CC Db 1 MSNVVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRCRMEASQKWK 60
XX CC
XX CC QY 61 NFDQNHKPLEGKYEWQVEKGSIPFFYYPPPPPKGACVKPAQESQDVSGSPFAAPLIG 120
XX CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX CC Db 61 NFDQNHKPLEGKYEWQVEKGSIPFFYYPPPPPKGACVKPAQESQDVSGSPFAAPLIG 120
XX CC
XX CC QY 121 AFANSEDLHLVDPKTDPSQDTGLAEQACAGIRKRPATDDSSSTONKRANRTEENVSDGSPN 180
XX CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX CC Db 121 AFANSEDLHLVDPKTDPSQDTGLAEQACAGIRKRPATDDSSSTONKRANRTEENVSDGSPN 180
XX CC
XX CC QY 181 AGSVEQTPKKPGLRRROT 198
XX CC ||||||||||||||||||
XX CC Db 181 AGSVEQTPKKPGLRRROT 198
XX CC
XX CC RESULT 4
XX CC AAY00768
XX CC ID AAY00768 standard; Protein: 198 AA.
XX CC AC AAY00768;
XX CC DT 14-MAY-1999 (first entry)
XX CC DE CKI/KIP protein p27.
XX CC KW CKI/KIP protein; p27 protein; cyclin kinase inhibitor; cancer;
XX CC KW hyperproliferative disorder
XX CC OS Homo sapiens.
XX CC PN W09904238-A2.
XX CC PD 28-JAN-1999.
XX CC PF 14-JUL-1998; 98WO-US14566.
XX CC PR 15-JUL-1997; 97US-09q3276
XX CC PA (DEAC-) DEACONESS HOSPITAL.
XX CC PA (MITO-) MITOTIX INC.
XX CC PI Draetta G, Loda M, Pagano M, Rolfe M;
XX CC WPI; 1999-132426/11.
XX CC DR N-PSDB; AAX21817
XX CC
```

```
PT PT Methods for diagnosis and prognosis of hyperproliferative disorders
PT PT - by determining the level of cyclin kinase inhibitor protein(s),
PT PT particularly p27
XX CC Claim 18; Page 36 37; 53pp; English.
XX CC
XX CC This sequence is the cyclin kinase inhibitor (CKI) protein p27. The
XX CC invention relates to a method for diagnosing a hyperproliferative
XX CC disorder, associated with the destabilisation of a CKI protein in cells
XX CC of a patient, comprises: (i) ascertaining the CKI protein level in a
XX CC sample of patient cells; and (ii) diagnosing the presence or absence of a
XX CC hyperproliferative disorder by utilising the ascertained CKI protein
XX CC level, where a reduced CKI protein level, relative to a normal control
XX CC cell sample, correlates with the presence of a hyperproliferative
XX CC disorder. The methods are useful for diagnosing disorders associated with
XX CC hyperproliferation, evaluating their aggressiveness and/or rate of
XX CC recurrence and as prognosis for evaluating a cancer patient's risk of
XX CC death. From the observations, treatment can be applied on the basis of
XX CC the patient's risk of death and/or recurrence of the cancer. The
XX CC diagnostic methods may also be employed as follow-up to treatment,
XX CC e.g. quantitation of the level of p27 protein may be indicative of the
XX CC effectiveness of current or previously employed cancer therapies as well
XX CC as the effect of these therapies upon patient prognosis. The methods and
XX CC reagents allow the detection of loss of p27 protein from a cell in order
XX CC to diagnose and phenotype proliferative disorders arising from
XX CC tumorigenic transformation of cells, or other hyperplastic or neoplastic
XX CC transformation processes as well as differentiative disorders such as
XX CC degeneration of tissue e.g. neurodegeneration.
XX CC
XX CC Sequence 198 AA;
XX CC
XX CC Query Match 100.0%; Score 1064; DB 20; Length 198;
XX CC Best Local Similarity 100.0%; Pred. No. 7.2e-100;
XX CC Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 1 MSNVVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRCRMEASQKWK 60
XX CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX CC Db 1 MSNVVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRCRMEASQKWK 60
XX CC
XX CC QY 61 NFDQNHKPLEGKYEWQVEKGSIPFFYYPPPPPKGACVKPAQESQDVSGSPFAAPLIG 120
XX CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX CC Db 61 NFDQNHKPLEGKYEWQVEKGSIPFFYYPPPPPKGACVKPAQESQDVSGSPFAAPLIG 120
XX CC
XX CC QY 121 APANSEDLHLVDPKTDPSQDTGLAEQACAGIRKRPATDDSSSTONKRANRTEENVSDGSPN 180
XX CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX CC Db 121 APANSEDLHLVDPKTDPSQDTGLAEQACAGIRKRPATDDSSSTONKRANRTEENVSDGSPN 180
XX CC
XX CC QY 181 AGSVEQTPKKPGLRRROT 198
XX CC ||||||||||||||||||
XX CC Db 181 AGSVEQTPKKPGLRRROT 198
XX CC
XX CC RESULT 5
XX CC AAY97523
XX CC ID AAY97523 standard; Protein: 198 AA.
XX CC AC AAY97523;
XX CC DT 15-JAN-2001 (first entry)
XX CC DE Human p27 protein sequence.
XX CC KW Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;
XX CC KW adenovirus E4 protein; neoplasia, p27 protein.
XX CC OS Homo sapiens.
XX CC PN W0200052184-A1.
XX CC PD 08-SEP-2000.
XX CC PF 01-MAR-2000; 2000WO-US05350.
XX CC
```



RESULT 7  
 AAY96066  
 ID AAY96066 standard; Protein: 198 AA.  
 AC AAY96066;  
 XX  
 XX  
 DT 05-DEC-2000 (first entry);  
 XX  
 XX  
 DE Human cyclin dependent kinase inhibitor p27.  
 DE Cyclin dependent kinase inhibitor; CDK1; KIP; human; p27;  
 KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
 KW endometriosis; psoriasis; vascular retinopathy; cytostatic;  
 KW antiarthritic; antirheumatic; gynaecological; antipsoriatic;  
 KW antiproliferative; gene therapy.  
 XX  
 OS Homo sapiens.  
 FH Key location/qualifiers  
 FI Domain 25..93 /note= "CDK inhibitory domain"  
 FI Domain 144..194 /note= "QT domain"  
 FI Peptide 152..166 /note= "nuclear localisation signal"  
 FI Modified-site 10..13 /note= "O phosphorylated; weak CDK phosphorylation site"  
 FI Modified-site 178..181 /note= "O-phosphorylated; phosphorylation site for proline-directed kinases"  
 FI Modified-site 187..190 /note= "O-phosphorylated; CDK phosphorylation consensus site"  
 XX  
 PN W0200052158-A1.  
 XX  
 PD 08-SEP-2000.  
 XX  
 XX 28-FEB-2000; 2000WO-0504970.  
 XX  
 PR 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 94US-0163682.  
 PR 09-DEC-1999; 94US-0457646.  
 XX  
 PA (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.  
 XX  
 PI Patel S, McArthur J, Gyuris J;  
 XX  
 DR WPI: 2000-565501/52.  
 DR N-PSDB: AAA50519.  
 XX  
 PT Inhibiting angiogenesis and treating angiogenesis-associated conditions, e.g. neoplasia, psoriasis by transducing an endothelial cell with a recombinant virus having a transgene encoding a cyclin dependent kinase inhibitor.  
 XX  
 PS Example 1; Page 127-128; 138pp; English.  
 XX  
 CC The present sequence is that of human p27, a cyclin dependent kinase inhibitor (CKI) that inhibits angiogenesis. A claimed method for inhibiting angiogenesis involves transducing an epithelial cell with a transgene encoding (internalizable, secretable) CKI. The delivery system for the transgene may be a liposome or a recombinant virus. The CKI is preferably a protein of the CIP/KIP family, such as p27, a protein of the INK4 family such as p16, active fragments of these proteins (e.g. amino acids 25-93 or 12-178 of human p27), or a fusion of 2 CKI proteins such as p27 and p16 (see AAY96066-80). The method is useful in treating conditions associated with angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis, psoriasis and vascular retinopathy.

CC (claimed). Alternatively, the transgene is delivered to an auxiliary cell, and is expressed by that cell such that the CDK1 is released into the blood and contacts the target epithelial cell.  
 XX  
 SO Sequence 198 AA;  
 Query Match 100.0%; Score 1064; DB 21; Length 198;  
 Best Local Similarity 100.0%; Pred No 7; 20-100;  
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSNVSVNSGSPSLPMAPQAEHPKPSACRNLFPGVDFHEFLTDLKHKFDMEEASQKRW 60  
 DB 1 MSNVSVNSGSPSLERMDAQAEHPKPSACRNLFPGVDFHEFLTDLKHKFDMEEASQKRW 60  
 QY 61 NFDFOHKKPLEGKYEWQVEKSLPEFYRPPPPKACKVPAQESQDVSGSPAPPLIG 120  
 DB 61 NFDFOHKKPLEGKYEWQVEKSLPEFYRPPPPKACKVPAQESQDVSGSPAPPLIG 120  
 QY 121 APANSEDIHLVDPKTPSPQSTGLAEQCCAGIRKPPATDSDSTONKKNRTEENVSDGSPN 180  
 DB 121 APANSEDIHLVDPKTPSPQSTGLAEQCCAGIRKPPATDSDSTONKKNRTEENVSDGSPN 180  
 QY 181 AGSVFQTPKKPKGLRRRQT 198  
 DB 181 AGSVFQTPKKPKGLRRRQT 198  
 RESULT 8  
 AAY44400  
 ID AAY44400 standard; Protein: 198 AA.  
 AC AAY44400;  
 XX  
 XX 22-MAR-2000 (first entry)  
 XX  
 DE Human p27(Kip1) kinase inhibitor protein.  
 XX  
 KW p27(Kip1) kinase inhibitor protein; FKBP 12, p27(Kip1), FKBP-12 complex; cytosolic drug-binding protein; yeast two hybrid assay system;  
 KW cell differentiation; apoptosis; neurodegeneration; tumorigenicity;  
 KW cell proliferation related disorder; atherosclerosis; autoimmune disease, transplant rejection; inflammation; allergy; cancer; viral infection;  
 KW membranous nephropathy; CDK; cyclin-dependent kinase.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FI Region 43..198 /note= "prey sequence that interacts with FKBP-12"  
 FT  
 FT  
 XX W09065930-A1  
 PN  
 XX 23-DEC-1999.  
 PD  
 XX  
 XX 18-JUN-1999; 99WO-US13659.  
 PF  
 XX 18-JUN-1998; 98US-0099857.  
 PR  
 XX  
 XX (CURA-) CURAGEN CORP  
 PA  
 XX Nandabalan K, Yang M;  
 PI  
 XX WPI: 2000-116763/10.  
 DR N-PSDB: AAZ29564.  
 XX  
 XX New complex of p27(Kip1) and FKBP-12 for treatment, prevention and diagnosis of, e.g. cancer and autoimmune disease.  
 PT  
 PS Claim 1; Fig 1; 78pp; English.  
 XX  
 CC The present sequence is p27(Kip1) kinase inhibitor protein. This protein requires CK1 activity by inhibiting cyclin-CK1 complex associated kinase activity. Interaction between p27(Kip1) and FKBP 12 (a cytosolic



XX The invention relates to methods of altering the polypeptide levels in a  
CC cell, using proteins selected from S-phase kinase associated proteins 1  
CC and 2 (SKP1, SKP2), SKP2 like proteins (2F) and CUL-1 (a member of the  
CC cullin/ CDC53 family of proteins). The method is useful for altering the  
CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
CC that modulate interactions between SKP and target proteins are useful for  
CC treating tumours.

XX SQ Sequence 198 AA.

Query Match 100.0%. Score 1064. DB 22; Length 198;  
Best Local Similarity 100.0%. Pred. No. 7.2e-100;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 MSNVRVNSGSPSLERMDARQAFHPKPSACRNLEFPGVDEHLETRDLKHKHCEASQKWK 60  
DB 1 MSNVRVNSGSPSLERMDARQAFHPKPSACRNLEFPGVDEHLETRDLKHKHCEASQKWK 60  
C 61 NFEQNHKPLEGRYEWQVEKGSLSPEFYYPFPKPKACKVFAGESQVSGSFAAPLIG 120  
DB 61 NFEQNHKPLEGRYEWQVEKGSLSPEFYYPFPKPKACKVFAGESQVSGSFAAPLIG 120  
QY 121 APANSEDTHLVDPKTPDSDSGTGLAEQACGIRKRPATDSDSTONKRNKTEENVSDGSPN 180  
DB 121 APANSEDTHLVDPKTPDSDSGTGLAEQACGIRKRPATDSDSTONKRNKTEENVSDGSPN 180  
QY 181 AGSVEQTPKKPLRRRQT 198  
DB 181 AGSVEQTPKKPLRRRQT 198

## RESULT 11

AAB47880  
ID AAB47880 standard; protein; 198 AA.  
XX AC AAB47880;  
XX DT 02-MAY-2002 (first entry)  
XX DE p27-Kip1.

XX Cell cycle inhibitor; antisense; inner ear; sensory hair cell;  
KW support cell; auditory function; hearing disorder;  
KW sensory neuronal hearing loss; SNHL.

XX Homo sapiens.  
XX W020204605 A2.  
XX 17-JAN 2002.  
XX 10-JUL-2001; 2001WC-0521793.  
XX 11-JUL-2000; 2000MS-0614099.  
XX (OTOG-) OTOGENE USA INC.  
XX (OTOG-) OTOGENE AG.

XX Kil J, Gu R, Griguer C, Lowenheim H;  
XX W01; 2002-171713/22.  
XX N-PSDB; AA172396.

XX Stimulating the formation of inner ear sensory hair cells, useful for  
PT treating hearing disorder involves damaging first inner ear sensory  
PT hair cells and promoting the formation of new sensory hair cells from  
PT inner ear support cells.

XX Disclosure: Page 64; 77pp; English.

PS  
XX

CC The sequences given in AAB47879-85 are cell cycle inhibitors. The nucleic  
CC acids encoding these proteins may be hybridised by antisense molecules in  
CC the method of the invention. The method is for stimulating the formation  
CC of an inner ear sensory hair cell from an inner ear support cell and  
CC involves damaging a first inner ear sensory hair cell under conditions  
CC that promote the formation of at least one inner ear sensory hair cell  
CC that is in contact with the damaged first inner ear hair cell.  
CC The method is useful for stimulating the formation of inner ear  
CC cells e.g. sensory hair cells and support cells, for improving an  
CC auditory function in an inner ear, in the treatment of hearing disorder  
CC e.g. sensory neuronal hearing loss (SNHL), to identify genes and/or  
CC proteins that are capable of stimulating the formation of inner ear  
CC sensory hair cells and/or the formation of inner ear support cells  
CC from sensory hair cells. The method damages and/or kills the inner  
CC ear sensory cells, such as sensory hair cells and support cells, which  
CC results in the increased stimulation in the formation of new, inner ear  
CC hair cells, thus resulting in the improved curing of the auditory  
CC function.

XX SQ Sequence 198 AA;

Query Match 100.0%. Score 1064. DB 23; Length 198;  
Best Local Similarity 100.0%. Pred. No. 7.2e-100;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSNVRVNSGSPSLERMDARQAFHPKPSACRNLEFPGVDEHLETRDLKHKHCEASQKWK 60  
QY 61 NFEQNHKPLEGRYEWQVEKGSLSPEFYYPFPKPKACKVFAGESQVSGSFAAPLIG 120  
DB 61 NFEQNHKPLEGRYEWQVEKGSLSPEFYYPFPKPKACKVFAGESQVSGSFAAPLIG 120  
QY 121 APANSEDTHLVDPKTPDSDSGTGLAEQACGIRKRPATDSDSTONKRNKTEENVSDGSPN 180  
DB 121 APANSEDTHLVDPKTPDSDSGTGLAEQACGIRKRPATDSDSTONKRNKTEENVSDGSPN 180  
QY 181 AGSVEQTPKKPLRRRQT 198  
DB 181 AGSVEQTPKKPLRRRQT 198

## RESULT 12

AAY70307  
ID AAY70307 standard; protein; 198 AA.  
XX AC AAY70307;  
XX DT 06-JUN-2000 (first entry)  
XX DE Human mutant cyclin-dependent kinase inhibitor (CKI), p27 S10A protein.  
XX KW Cyclin-dependent kinase inhibitor; CKI; p27; human; mutant; G1 phase;  
KW KIS; serine/threonine kinase; cell proliferation; modulator; treatment;  
KW cell proliferative disease, vascular disorder, gene therapy; restenosis;  
KW atherosclerosis.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 10 /note= "wild type Ser substituted with Ala"

XX W020001165-A1.

XX 02-MAR-2000.

XX 20-AUG-1999; W000-0518403.

XX 21-AUG-1998; 980S-0697710

XX (NABE/) NABEL G J.

XX (NABE/) NABEL E G.









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OM protein - protein search, using sw model

Run on: May 30, 2003 08:55:37 - Search time 14.8372 seconds  
(without alignments)  
392 644 Million on-line updates/sec

Title: US-09-865-018B-2  
Perfect score: 1054  
Sequence: 1 MSNVFVNSGSPSLERMEAFQAEHKPSA

Scoring table: RUSUM62  
GapPen 10 6 0 GapExt 0 6  
PNA:USVPL3PKKPLPPPPPT 194

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 260000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /seqn2\_6/ptedata/1/1aa/6C\_10MB.ppf.\*  
6: /seqn2\_6/ptedata/1/1aa/6D\_10MB.ppf.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1064	100.0	198	1	US-08-406-248-4
2	1064	100.0	198	4	US-08-897-333A-2
3	1064	100.0	198	4	US-09-240-006-6
4	1064	100.0	198	4	US-08-794-002-2
5	1064	100.0	198	4	US-08-457-568-24
6	1064	100.0	198	4	US-08-457-568-24
7	1059	99.5	391	1	US-08-589-981-2
8	1059	99.5	391	4	US-09-457-568-4
9	1059	99.5	391	4	US-09-457-646-4
10	1057	99.3	198	1	US-08-275-983B-3
11	1054	99.1	365	4	US-08-457-568-16
12	1054	99.1	365	4	US-08-457-646-16
13	1054	99.1	380	4	US-09-457-568-8
14	1054	99.1	380	4	US-09-457-646-8
15	1052	98.5	158	4	US-08-453-036-2
16	1047	98.4	365	4	US-09-457-568-6
17	1047	98.4	365	4	US-09-457-646-6
18	933	87.7	197	3	US-08-415-655-6
19	931	87.5	197	1	US-08-275-983B-2
20	931	87.5	197	4	US-09-240-006-8
21	931	87.5	197	4	US-09-415-421-57
22	931	87.5	197	4	US-08-794-002-4
23	928	87.2	197	4	US-08-854-034R-4
24	908	85.3	334	4	US-09-457-568-16
25	908	85.3	334	4	US-09-457-646-16
26	906.5	85.2	348	4	US-09-457-568-14
27	906.5	85.2	348	4	US-09-457-646-14

28	900.5	84.6	195	4	US-08-415-221-54
29	900	84.6	177	4	US-08-457-568-12
30	900	84.6	177	4	US-08-457-646-12
31	895	84.2	212	4	US-09-215-221-49
32	885	83.2	194	4	US-09-215-221-52
33	884	83.1	194	4	US-09-215-221-53
34	874	82.1	194	4	US-09-215-221-51
35	870	81.8	178	4	US-08-794-002-6
36	870	81.8	178	4	US-08-854-034R-6
37	870	81.8	198	4	US-08-275-983B-1
38	870	81.8	198	4	US-08-794-002-22
39	837	78.7	180	4	US-09-215-221-55
40	833	78.3	180	4	US-09-215-221-50
41	834	78.3	135	4	US-08-415-421-56
42	404	38.0	323	4	US-09-457-646-30
43	403	37.9	247	4	US-08-457-568-20
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45	401	37.7	252	4	US-09-457-568-22

ALIGNMENTS

RESULT 1  
US-08-406-248-4  
Sequence 4, Application US/08406248  
Patent No. 5736318  
GENERAL INFORMATION:  
APPLICANT: Mungier, Karl  
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING  
TITLE OF INVENTION: TRANSFORMED CELLS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ann-Louise Kermer, Ph.D., Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER RELEVABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/406,248  
FILING DATE:  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniels, Patricia A.  
REGISTRATION NUMBER: 33,194  
REFERENCE/DOCKET NUMBER: HAZ-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 198 amino acids  
TYPE: amino acid  
Topology: linear  
MOLECULE TYPE: protein  
US-08-406-248-4

Query Match	100.0%	Score 1064	DB 1	Length 198
Best local Similarity	100.0%	Pred No 2	1e-103	
Matches 198	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MSNVFVNSGSPSLERMDARQAEHKPSACPNLFPGVPIHKLTPDLKHKHCKHMEEASQKRW	60	
Db	1	MSNVFVNSGSPSLERMDARQAEHKPSACPNLFPGVPIHKLTPDLKHKHCKHMEEASQKRW	60	
Qy	61	NFDGNHKPLGCKYENQVEKSGSLPEFYFRPPKPKGACKVPAQESQDYSQSRPAAPLIC	120	



Db 61 NFDQNHKPLEGKYEWQVEKGSLEPFFYRPPPKGACKVPAQESQDVSGSRPAAPLIG 120  
QY 121 APANSEDLHLVDPKTPDSUSQTGLAQCGAGIRKPKPATDSSSTQNKRNKTEENVSDGSPN 180  
Db 121 APANSEDLHLVDPKTPDSUSQTGLAQCGAGIRKPKPATDSSSTQNKRNKTEENVSDGSPN 180  
QY 181 AGSVEQTPKKPLRRQQT 198  
Db 181 AGSVEQTPKKPLRRQQT 198

## RESULT 5

US-09-457-568-26  
: Sequence 26, Application US/09457568  
: Patent No. 6413943  
: GENERAL INFORMATION:  
: APPLICANT: McArthur, James G  
: APPLICANT: Gyuris, Jeno  
: APPLICANT: Finer, Mitchell H  
: TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of  
: TITLE OF INVENTION: Smooth Muscle Cells  
: FILE REFERENCE: 106482.691  
: CURRENT APPLICATION NUMBER: US/09/457,568  
: CURRENT FILING DATE: 1999-12-09  
: EARLIER APPLICATION NUMBER: 60/122,974  
: EARLIER FILING DATE: 1999-03-01  
: EARLIER APPLICATION NUMBER: 60/153,682  
: EARLIER FILING DATE: 1999-11-05  
: NUMBER OF SEQ ID NOS: 28  
: SOFTWARE: Patent In Ver. 2.0  
: SEQ ID NO 26  
: LENGTH: 198  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-457-568-26

Query Match 100.0%; Score 1064; DB 4; Length 198;  
Best Local Similarity 100.0%; Pred. No. 2 1e-103;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSNVVNSGSPSLERMDARQAEHPKPSACRNLPFGVDHEELTRDLEKHCRDMEASQKWK 60  
Db 1 MSNVVNSGSPSLERMDARQAEHPKPSACRNLPFGVDHEELTRDLEKHCRDMEASQKWK 60  
QY 61 NFDQNHKPLEGKYEWQVEKGSLEPFFYRPPPKGACKVPAQESQDVSGSRPAAPLIG 120  
Db 61 NFDQNHKPLEGKYEWQVEKGSLEPFFYRPPPKGACKVPAQESQDVSGSRPAAPLIG 120  
QY 121 APANSEDLHLVDPKTPDSUSQTGLAQCGAGIRKPKPATDSSSTQNKRNKTEENVSDGSPN 180  
Db 121 APANSEDLHLVDPKTPDSUSQTGLAQCGAGIRKPKPATDSSSTQNKRNKTEENVSDGSPN 180  
QY 181 AGSVEQTPKKPLRRQQT 198  
Db 181 AGSVEQTPKKPLRRQQT 198

## RESULT 6

US-09-457-646-26  
: Sequence 26, Application US/09457646  
: Patent No. 6420345  
: GENERAL INFORMATION:  
: APPLICANT: Patel, Sallil P  
: APPLICANT: McArthur, James G  
: APPLICANT: Gyuris, Jeno  
: TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of  
: TITLE OF INVENTION: Smooth Muscle Cells  
: FILE REFERENCE: 106482.287  
: CURRENT APPLICATION NUMBER: US/09/457,646  
: CURRENT FILING DATE: 1999-12-09  
: EARLIER APPLICATION NUMBER: 60/122,974  
: EARLIER FILING DATE: 1999-03-01

: EARLIER APPLICATION NUMBER: 60/163,682  
: EARLIER FILING DATE: 1999-11-05  
: NUMBER OF SEQ ID NOS: 32  
: SOFTWARE: Patent In Ver. 2.0  
: SEQ ID NO 26  
: LENGTH: 198  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-457-646-26

Query Match 100.0%; Score 1064; DB 4; Length 198;  
Best Local Similarity 100.0%; Pred. No. 2 1e-103;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSNVVNSGSPSLERMDARQAEHPKPSACRNLPFGVDHEELTRDLEKHCRDMEASQKWK 60  
Db 1 MSNVVNSGSPSLERMDARQAEHPKPSACRNLPFGVDHEELTRDLEKHCRDMEASQKWK 60  
QY 61 NFDQNHKPLEGKYEWQVEKGSLEPFFYRPPPKGACKVPAQESQDVSGSRPAAPLIG 120  
Db 61 NFDQNHKPLEGKYEWQVEKGSLEPFFYRPPPKGACKVPAQESQDVSGSRPAAPLIG 120  
QY 121 APANSEDLHLVDPKTPDSUSQTGLAQCGAGIRKPKPATDSSSTQNKRNKTEENVSDGSPN 180  
Db 121 APANSEDLHLVDPKTPDSUSQTGLAQCGAGIRKPKPATDSSSTQNKRNKTEENVSDGSPN 180  
QY 181 AGSVEQTPKKPLRRQQT 198  
Db 181 AGSVEQTPKKPLRRQQT 198

## RESULT 7

US-08-589-981-2  
: Sequence 2, Application US/08589981  
: Patent No. 5672508  
: GENERAL INFORMATION:  
: APPLICANT: Gyuris, Jeno  
: APPLICANT: Lamphere, Lou  
: APPLICANT: Beach, David H.  
: TITLE OF INVENTION: Inhibitors of Cell-Cycle Progression,  
: TITLE OF INVENTION: and Uses Related Thereto  
: NUMBER OF SEQUENCES: 4  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: LAHIVE & COCKFIELD  
: STREET: 60 State Street  
: CITY: Boston  
: STATE: MA  
: COUNTRY: USA  
: ZIP: 02109  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: ASCII (text)  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/589,981  
: FILING DATE:  
: CLASSIFICATION: 530  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Vincent, Matthew P.  
: REGISTRATION NUMBER: 36,709  
: REFERENCE/DOCKET NUMBER: MII-069  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (617) 227-7400  
: TELEFAX: (617) 227-5941  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 391 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
US-08-589-981-2



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: REFERENCE (7) = VET NIMREP: M11-0700P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)227-5941
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 198 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: Internal
: US-08-275-983B-3

Query Match
Best Local Similarity: 99.3%, Score 1057, DB 1, Length 198;
Matches 196; Conservative 2, Mismatches 0, Indels 0, Gaps 0;

QY 1 MSNVVNSGSPSLERMDARQAEHPKPSACRNLFPGVDHFEITRLEKHCHPDMEEASQPKWN 60
Db 1 MSNVVNSGSPSLERMDARQAEHPKPSACRNLFPGVDHFEITRLEKHCHPDMEEASQPKWN 60
QY 61 NFDQNHKPLEGKYEWEVEKGSUPEFYRPPKCKACKVPAQESQDVSGSRPAAPLIG 120
Db 61 NFDQNHKPLEGKYEWEVEKGSUPEFYRPPKCKACKVPAQESQDVSGSRPAAPLIG 120
QY 121 AFANSECTHLVDPKIDFSQVIGLAQCAGIRKKPATDSDSTQNKANKRTEENVSDGSPN 180
Db 121 AFANSECTHLVDPKIDFSQVIGLAQCAGIRKKPATDSDSTQNKANKRTEENVSDGSPN 180
QY 181 AGSVETPKKPGIAPPQT 198
Db 181 AGSVETPKKPGIAPPQT 198

RESULT 11
US-09-457-568-10
: Sequence 10, Application US/09457568
: Patent No. 6413943
: GENERAL INFORMATION:
: APPLICANT: McArthur, James G
: APPLICANT: Gyuris, Jeno
: APPLICANT: Finer, Mitchell H
: TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
: TITLE OF INVENTION: Smooth Muscle Cells
: FILE REFERENCE: 106482.691
: CURRENT FILING DATE: 1999-12-09
: EARLIER FILING DATE: 1999-03-01
: EARLIER APPLICATION NUMBER: 60/122,974
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 10
: LENGTH: 365
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-457-568-10

Query Match
Best Local Similarity: 99.1%, Score 1054, DB 4, Length 365,
Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SNVSVNSGSPSLERMDARQAEHPKPSACRNLFPGVDHFEITRLEKHCHPDMEEASQPKWN 61
Db 169 SNVSVNSGSPSLERMDARQAEHPKPSACRNLFPGVDHFEITRLEKHCHPDMEEASQPKWN 228
QY 62 FDFONHKLPGKYEWEVEKGSUPEFYRPPKCKACKVPAQESQDVSGSRPAAPLIG 121
Db 229 FDFONHKLPGKYEWEVEKGSUPEFYRPPKCKACKVPAQESQDVSGSRPAAPLIG 288
QY 122 PANSEDTHLVDPKIDFSQVIGLAQCAGIRKKPATDSDSTQNKANKRTEENVSDGSPN 181
Db 289 PANSEDTHLVDPKIDFSQVIGLAQCAGIRKKPATDSDSTQNKANKRTEENVSDGSPN 348
QY 182 GSVETPKKPGIAPPQT 198
Db 349 GSVETPKKPGIAPPQT 465

RESULT 13
US-09-457-568-8
: Sequence 8, Application US/09457568
: Patent No. 6413943
: GENERAL INFORMATION:
: APPLICANT: McArthur, James G
: APPLICANT: Gyuris, Jeno
: APPLICANT: Finer, Mitchell H
: TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
: TITLE OF INVENTION: Smooth Muscle Cells
: FILE REFERENCE: 106482.691
: CURRENT FILING DATE: 1999-12-09
: EARLIER FILING DATE: 1999-03-01
: EARLIER APPLICATION NUMBER: 60/122,974
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 8
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[illegible]

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1  RESULT 14
2  US 09 457 646, A
3  : Sequence of Application US/09/457646
4  : Patent No. 6420446
5  : GENERAL INFORMATION:
6  : APPLICANT: Parol, Sall D
7  : APPLICANT: McArthur, James G
8  : APPLICANT: Gyuris, Gern
9  : TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
10 : TITLE OF INVENTION: Smooth Muscle Cells
11 : FILE REFERENCE: 196492.287
12 : CURRENT APPLICATION NUMBER: 09/457,646
13 : CURRENT FILING DATE: 1999-12-09
14 : EARLIER APPLICATION NUMBER: 63/122,974
15 : EARLIER FILING DATE: 1999-04-01
16 : EARLIER APPLICATION NUMBER: 63/161,682
17 : EARLIER FILING DATE: 1999-11-05
18 : NUMBER OF SEQ. IN SEQ.: 42
19 : SOFTWARE: Patent In Ver. 2.0
20 : SEQ. ID NO.: 9
21 : LENGTH: 880
22 : TYPE: PRT
23 : ORGANISM: Homo Sapiens

```

[illegible]

US 08-054 039B-2  
Sequence 2, Application US/08B54039A  
Patent No. 6,555,774  
GENERAL INFORMATION:  
APPLICANT: Massague, Joaqui  
APPLICANT: Roberts, James M.  
APPLICANT: Koff, Andrew  
APPLICANT: Polvak, Kordelia  
TITLE OF INVENTION: ISOLATED PZ1 PROTEIN AND METHOD FOR ITS  
TITLE OF INVENTION: ISOLATED PZ1 PROTEIN AND METHOD FOR ITS  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELLIOTT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-4170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.40  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 05/08/954, 039B  
FILING DATE: 09 MAY 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/PATENT NUMBER: MIV 079, 04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-852-1090  
TELEFAX: 617-852-7000  
INFORMATION FOR SEQUENCE:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US 08-054 039B-2

[illegible]

Search completed: May 50, 2005, 09:03:4.





```

RESULT 2
US 08 902 572 2
Sequence 2, Application US/08902572
Patent No. US20020068706A1
GENERAL INFORMATION:
APPLICANT: Gyuris, Jono
APPLICANT: Lamprecht, Jon
APPLICANT: Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: POLLEY, HOWE & ELLIOT LLP
STREET: one Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109 2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: pc dos/MS dos
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
FILING DATE: 29 JUL 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/CKET NUMBER: MIV 069,034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 842 1000
TELEFAX: 617 842 7000
INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
Topology: linear
MOLECULE TYPE: protein
US 08 902 572 2

Query Match 99.9% Score 1059; DB 8; Length 491;
Best Local Similarity 100.0%; Pred. No. 14e B3;
Matches 197; Conservative 0; Mismatches 0; Gaps 0;

QY 2 SNVSVNSISLERMDARQALHPRKNA*KNLEGLVDFDELIDLEKHPKOMEASQKWN 61
DB 8 SVYVNSISLERMDARQALHPRKNA*KNLEGLVDFDELIDLEKHPKOMEASQKWN 61
QY 62 FDFQNHKEPEKYEYEWVEKESIFRYEYEPPEPPKGA*KVIAQSSQVSSSRPAAPLGA 121
DB 6 FDFQNHKEPEKYEYEWVEKESIFRYEYEPPEPPKGA*KVIAQSSQVSSSRPAAPLGA 121
QY 122 PARSELHVLVETLLEHGGELALFACIKERATLAGEHJNKEANETERNVSGSSNA 181
DB 122 PARSELHVLVETLLEHGGELALFACIKERATLAGEHJNKEANETERNVSGSSNA 181
QY 289 FANSEHDLVDFKIDPSQSGALQKAGIKPRATDISSIQNKRANPTRENVSGSSNA 348
DB 289 FANSEHDLVDFKIDPSQSGALQKAGIKPRATDISSIQNKRANPTRENVSGSSNA 348
QY 162 GSVEQTPKPKLRRPQT 198
DB 162 GSVEQTPKPKLRRPQT 198
QY 188 GSVEQTPKPKLRRPQT 204
DB 188 GSVEQTPKPKLRRPQT 204

RESULT 3
US 08 902 572 8
Sequence 8, Application US/08902572
Patent No. US20020068706A1
GENERAL INFORMATION:
APPLICANT: Gyuris, Jono
APPLICANT: Lamprecht, Jon
APPLICANT: Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: POLLEY, HOWE & ELLIOT LLP
STREET: one Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109 2170

```

```

TITLE OF INVENTION: INHIBITORS OF CELL CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: POLLEY, HOWE & ELLIOT LLP
STREET: one Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109 2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: pc dos/MS dos
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
FILING DATE: 29 JUL 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/CKET NUMBER: MIV 069,034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 842 1000
TELEFAX: 617 842 7000
INFORMATION FOR SEQ ID NO: 8;
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
Topology: linear
MOLECULE TYPE: protein
US 08 902 572 8

Query Match 99.1% Score 1054; DB 8; Length 465;
Best Local Similarity 99.5%; Pred. No. 45e B4;
Matches 196; Conservative 1; Mismatches 1; Gaps 0;

QY 2 SNVSVNSISLERMDARQALHPRKNA*KNLEGLVDFDELIDLEKHPKOMEASQKWN 61
DB 169 SVYVNSISLERMDARQALHPRKNA*KNLEGLVDFDELIDLEKHPKOMEASQKWN 228
QY 62 FDFQNHKEPEKYEYEWVEKESIFRYEYEPPEPPKGA*KVIAQSSQVSSSRPAAPLGA 121
DB 62 FDFQNHKEPEKYEYEWVEKESIFRYEYEPPEPPKGA*KVIAQSSQVSSSRPAAPLGA 121
QY 289 FANSEHDLVDFKIDPSQSGALQKAGIKPRATDISSIQNKRANPTRENVSGSSNA 348
DB 289 FANSEHDLVDFKIDPSQSGALQKAGIKPRATDISSIQNKRANPTRENVSGSSNA 348
QY 162 GSVEQTPKPKLRRPQT 198
DB 162 GSVEQTPKPKLRRPQT 198
QY 188 GSVEQTPKPKLRRPQT 204
DB 188 GSVEQTPKPKLRRPQT 204

RESULT 4
US 08 902 572 6
Sequence 6, Application US/08902572
Patent No. US20020068706A1
GENERAL INFORMATION:
APPLICANT: Gyuris, Jono
APPLICANT: Lamprecht, Jon
APPLICANT: Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: POLLEY, HOWE & ELLIOT LLP
STREET: one Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109 2170

```





Db 72 GYEWQVEKSGSLPEFYFPPPPKPKGATKVAQESQIVSGSPPAAPLIGANSEEDTHLV 131  
QY 132 DKTDPDSQSLAEQACGKPKPATGSSSTONKPKANFTENVS... --GSNAG 182  
Db 132 DKTDPDSQSLAEQACGKPKPATGSSSTONKPKANFTENVS... 131  
QY 183 SVE 185  
Db 192 SVE 194

## RESULT 9

US-08-902-572-18  
Sequence 18, Application US/08902572  
Patent No. US20020068706A1  
GENERAL INFORMATION:  
APPLICANT: Gyuris, Jeno  
APPLICANT: Lamphere, Lou  
APPLICANT: Beach, David H.  
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND  
TITLE OF INVENTION: RELATED THEREPTO  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.40  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,572  
FILING DATE: 23-JUL-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-069.03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 167 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-902 572 18

Query Match 84.6%; Score 900; DB A; Length 167;  
Best Local Similarity 100.0%; Pred No 2 6e-70;  
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SLERMLAQAEHPKPSACRNLFQPVUHELTGKHCRCMFEEASQKWNDFGNHKKPLE 71  
Db 2 SLERMLAQAEHPKPSACRNLFQPVUHELTGKHCRCMFEEASQKWNDFGNHKKPLE 61  
QY 72 GYEWQVEKSGSLPEFYFPPPPKPKGATKVAQESQIVSGSPPAAPLIGANSEEDTHLV 131  
Db 62 GYEWQVEKSGSLPEFYFPPPPKPKGATKVAQESQIVSGSPPAAPLIGANSEEDTHLV 121  
QY 132 DKTDPDSQSLAEQACGKPKPATGSSSTONKPKANFTENVS... 131  
Db 122 DKTDPDSQSLAEQACGKPKPATGSSSTONKPKANFTENVS... 127

## RESULT 10

US-09-865-018-6

Sequence 5, Application US/09865018  
Patent No. US20020110886A1  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Roberts, James M.  
APPLICANT: Koff, Andrew  
APPLICANT: Polyak, Kornelia  
TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS  
PRODUCTION AND USE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/865,018  
FILING DATE: 24-May-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,049  
FILING DATE: 09-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-079 04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-865-018-6

Query Match 81.8%; Score 870; DB 10; Length 178;  
Best Local Similarity 91.0%; Pred. No. 1 1e-67;  
Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MSNVVNSGSPSLERMLAQAEHPKPSACRNLFQPVUHELTGKHCRCMFEEASQKWNDFGNHKKPLE 50  
Db 1 MSNVVNSGSPSLERMLAQAEHPKPSACRNLFQPVUHELTGKHCRCMFEEASQKWNDFGNHKKPLE 60  
QY 61 NTFQNHKKPLESKYEWQVEKSGSLPEFYFPPPPKPKGATKVAQESQIVSGSPPAAPLIG 120  
Db 61 NTFQNHKKPLESKYEWQVEKSGSLPEFYFPPPPKPKGATKVAQESQIVSGSPPAAPLIG 120  
QY 121 APANSEATHLVKPKTIPKTHSQTGLAEQACGKPKPATGSSSTONKPKANFTENVS... 178  
Db 121 APANSEATHLVKPKTIPKTHSQTGLAEQACGKPKPATGSSSTONKPKANFTENVS... 178

## RESULT 11

US-08-902-572-26  
Sequence 26, Application US/08902572  
Patent No. US20020068706A1  
GENERAL INFORMATION:  
APPLICANT: Gyuris, Jeno  
APPLICANT: Lamphere, Lou  
APPLICANT: Beach, David H.  
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND  
TITLE OF INVENTION: RELATED THEREPTO  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:

```

ADDRESS: FLEY, HOWARD LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
MEDIUM TYPE: Floppy disk
COMPILED: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 35756/9-2-5/2
FILING DATE: 29 JUL 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 46,709
REFERENCE/KEY NUMBER: RIV 069 004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 862 7000
TELEFAX: 617 862 7000
INFORMATION CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS:
COUNTRY: United
Molecule type: peptide
US 08 502 5/2 28

Query Match
Best Match Similarity 47.9% Score 403 LR 81 Length 247
Matches 87 Conservative 9 Mismatches 39 Indexes 38 Gaps 4
C7 22 EBBKSAQPNFVGHVETTRFKRPFMPFASQPKNNFPCNRPKLEKGVQVEVER 81
14 9 DYASCSQENQGVGHVETTRFKRPFMPFASQPKNNFPCNRPKLEKGVQVEVER 68
C7 92 CSUPEYVROR PIRACKVAQE S2QV SASFAP 117
14 99 NSLFEYVRPRVPRVPAVSSMELSAWLAIAAGVGVRALEACALNAP 122

RESULT 14
US 08 502 5/2 28
Score 260 Application US/0606252
Patent No. US2002006706A1
GENERAL INFORMATION:
APPLICANT: Synthes, Jono
APPLICANT: Lamphrey, Don
APPLICANT: Beach, David H.
TITLE OF INVENTION: EXPANDED COMPLEX WIRE FRAME IN AN
TITLE OF INVENTION: RELATED THEREO
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEY, HOWARD LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPILED: IBM PC compatible
MEDIUM TYPE: Floppy disk
COMPILED: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
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INFORMATION CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS:
COUNTRY: United
Molecule type: peptide
US 08 502 5/2 20

```

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INFORMATION CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS:
COUNTRY: United
Molecule type: peptide
US 08 502 5/2 28

Query Match
Best Match Similarity 50.0% Score 403 LR 81 Length 247
Matches 87 Conservative 9 Mismatches 39 Indexes 38 Gaps 4
C7 22 EBBKSAQPNFVGHVETTRFKRPFMPFASQPKNNFPCNRPKLEKGVQVEVER 81
14 9 DYASCSQENQGVGHVETTRFKRPFMPFASQPKNNFPCNRPKLEKGVQVEVER 68
C7 92 CSUPEYVROR PIRACKVAQE S2QV SASFAP 117
14 99 NSLFEYVRPRVPRVPAVSSMELSAWLAIAAGVGVRALEACALNAP 122

RESULT 14
US 08 502 5/2 28
Score 260 Application US/0606252
Patent No. US2002006706A1
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APPLICANT: Lamphrey, Don
APPLICANT: Beach, David H.
TITLE OF INVENTION: EXPANDED COMPLEX WIRE FRAME IN AN
TITLE OF INVENTION: RELATED THEREO
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEY, HOWARD LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPILED: IBM PC compatible
MEDIUM TYPE: Floppy disk
COMPILED: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 35756/9-2-5/2
FILING DATE: 29 JUL 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 46,709
REFERENCE/KEY NUMBER: RIV 069 004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 862 7000
TELEFAX: 617 862 7000
INFORMATION CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS:
COUNTRY: United
Molecule type: peptide
US 08 502 5/2 20

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Query Match      37.6%, Score 394, DB 8, Length 70,
Best Local Similarity 100.0%, Pred. No. 3, 76-27,
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

25 KPSAQNPIFGVTHHEETIPQLEKRTMTFASQKWNFIPLNHHKPLEKYEWVEVKGSL 84
|||||
2 KPSACRNLEGVTHHEETIPQLERHTMTFASQKWNFIPLNHHKPLEKYEWVEVKGSL 61

85 PFEEYYPDP 93
|||||
62 PFEEYYPDP 79

```

```

RESULT 14
US-09 925 297 770
; Sequence 770, Affiliation US/09025297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US03/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,470
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 770
; LENGTH: 247
; TYPE: FRI
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (131)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-770

```

```

Query Match      16.5%: Score 175.5: DB 10: Length 247:
Best Local Similarity 29.8%: Pred. No. 1.2e-07:
Matches 59: Conservative 20: Mismatches 64: Indels 55: Gaps 9:

3  NRVASNGSPSLBMTAQAQAEHPKPCACENLFGPDVDEELTPDLEKHCHRDMEEFASORKWF 62
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
84  HVTGWCQS-----EPMPHKACPLPGPVTSFLSPFCIALMAGCLOAREXKNP 134
63  DFONHKPIEKKYFWGEVGSLEPIRYYPHPHPKAKVPAQESQLVSSGPPAAPLIGAP 122
      |||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
135  DFVETPLEGDFAWERVGLGFLKYL-----PLG---PKKGDELGGGR----- 176
123  ANSELDTHI VTPKTPPSISLTGLAEVAGLKKHPATU--DSSLNKKPARRTEENVSDGSPN 180
      ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
177 -----EPRTSPALD-ETAE-----DHWLDSLTCLVPPSGEQ_AEGSPG 215
181  AGSVEQTPKPKGLRRQOT 198
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
216  GPQDSQ-----GPRROT 228
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

```

RESULT 15  
 US-09-221-268-3  
 : Sequence 3, Application 02/05221268A  
 : Publication NO. US20020183509A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Fisher, Paul B. and  
 : APPLICANT: Jiang, Hongping  
 : APPLICANT: The Trustees of Columbia University in the City of New York  
 : TITLE OF INVENTION: METHOD FOR GENERATING A SURTRACTED CDNA LIBRARY AND  
 : TITLE OF INVENTION: USES OF THE GENERATING LIBRARY  
 : FILE REFERENCE: 0575/44563-B  
 : CURRENT APPLICATION NUMBER: US-09/221-268A

```

; CURRENT FILING DATE: 1998-12-23
; EARLIER APPLICATION NUMBER: 08/316,537
; EARLIER FILING DATE: 1994-09-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 3
; LENGTH: 164
; TYPE: PRT
; ORGANISM: MUA-6(2)
US-09-221-268-3

Query Match      16.1% Score 171.5; DB 9; Length 164.
Best Local Similarity 31.4%; Pred No 16e-07;
Matches 58; Conservative 20; Mismatches 58; Indels 49; Gaps 10;

              QY          Db          17 LAKAQAEHKPS-AACKNLGCPVDHEELTKULEKHCKDMEEASOKKWNFDQNHKPLEGKYE 75
              QY          Db          7 DVPQ--NPGSKACPPLEGVDSGLSPDCALMAGCTQFAPEPNWDFVTETPLGGDPA 64
              QY          Db          76 WUEVEKGSLPERRYKFPAPPKCAKVAQESDVVSQSRPAALICAPANSEDTHLVDPKT 135
              Db          65 WEVPWGILPKLYL-----PTG---PRGPDIEGGGP-----RPGT 97
              QY          Db          136 DPSTQSMTIAEQACAIKPAPTAT--TSQTQNKRANRIENVSUDGSFNAGSVEQIPKKPL 193
              Db          98 SFALLQ-NTAEE-----DHVELSLSLTLVPFSSQE-QAESNGCGIUSQ-----GR 140
              QY          Db          194 PRQT 198
              Db          141 KRQT 145

Search completed: May 10, 2003, 09:05:04
Job time : 21.2093 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd

OM protein - protein search, using sw model

Run on: May 30, 2003, 06:54:42, Search time: 39.479 seconds  
(without alignments) 1144.739 Million cell updates/sec

Title: US-09-865-018b-2

Perfect score: 1064

Sequence: 1 MSNVPSVNSPSLEFMDAPQ PNAQSVETPKKPLPPROT 198

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 9614122 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum BP seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Prof % is the ratio of hits its predicted by than it have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1054	99.1	198	2 152718	gene p27kip1 prote
2	921	87.5	197	2 149064	cyclin-cdk inhibit
3	220.5	20.7	216	2 392424	cyclin-dependent k
4	218	20.5	210	2 151683	cyclin-dependent k
5	212.5	20.0	418	2 153263	cyclin-cdk inhibit
6	191	18.0	164	2 184725	tumor suppressor p
7	179.5	16.5	155	2 143623	tumor suppressor p
8	176.5	16.6	143	2 A49438	p53 tumor suppress
9	172.5	16.2	121	2 168674	cyclin-dependent k
10	170.5	16.0	181	2 154380	cyclin-dependent k
11	151.5	14.2	258	2 124499	hypothetical prote
12	155	11.7	184	2 124496	hypothetical prote
13	100	9.4	191	2 101132	cyclin-dependent k
14	95	8.9	399	2 106522	paired type homeod
15	95	8.9	735	2 844147	alpha aducrin - ra
16	95	8.9	1173	2 142719	TPR-containing/SH2
17	94	8.8	246	1 S49770	hypothetical prote
18	94	8.8	856	2 116543	hypothetical prote
19	93.5	8.8	1307	2 117453	ERG-associated pro
20	93	8.7	403	2 147621	basic transcription
21	92	8.5	439	2 B44774	hypothetical prote
22	91.5	8.6	1076	2 S44764	C27D11.1 protein -
23	90.5	8.5	256	2 148401	histone deacetylase
24	90	8.5	913	2 B47369	translation initia
25	89	8.5	913	2 A82587	translation initia
26	89.5	8.4	515	2 T05863	hypothetical prote
27	89	8.4	611	1 S12766	translation initia
28	89	8.4	1211	2 142230	AP4 protein - mous
29	88.5	8.3	388	1 Q9YV	transforming prote

ALIGNMENTS

RESULT 1

152718

gene p27kip1 protein - human

C:Species: Homo sapiens (man)

C>Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000

C:Accession: I52718

R:Pietenpol, J A.; Rohlander, S K.; Sato, Y.; Papadopoulos, N.; Liu, B.; Friedman, C.

Cancer Res. 55, 1206-1210, 1995

A:Title: Assignment of the human p27kip1 gene to 12p13 and its analysis in leukemias.

A:Reference number: I52718; MUID:95188144; PMID:7882309

A:Accession: I52718

A:Status: preliminary; translated from GB/EMBL/DDJB

A:Molecule type: DNA

A:Residues: 1-198 -RES-

A:Cross references: GR S76988; NIH:3498402; PIR: AAL144.1; IID 34291944

C:Genetics:

A:Gene: p27kip1

A:Introns: 159/1

Query Match

Best Local Similarity 99.1%; Score 1054; DB 2; Length 198;

Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

57 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

58 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

59 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

60 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

61 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

62 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

63 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

64 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

65 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

66 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

67 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

68 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

69 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

70 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

71 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

72 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

73 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

74 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

75 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

76 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

77 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

78 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

79 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

80 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

81 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

82 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

83 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

84 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

85 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

86 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

87 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

88 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

89 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60

90 1 MSNVPSVNSPSLEFMDAPQAEHPKPSACFNLEFSPVDHEELTPGLEKHPDMEESQKWK 60











GenCore version 5.1.6  
Copyright (c) 1993-2003 Compugen Ltd.

OM protein protein search, using sw model

Run on: May 30, 2003, 08:52:42, Search time: 844:86, Scores  
(without alignments)  
972.808 Million cell updates/sec

Title: us-09-865-018b-2  
Perfect score: 1064  
Sequence: 1 MSNVRVNGSPSLERMDAPQ.....PNAGSVFQTPKKPCPLPPPT 198

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2899999999

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DR	ID	Description
1	1064	100.0	198	1	CDNB_HUMAN	P46527 homo sapien
2	994	93.4	198	1	CDNB_FELCA	O19001 felis silve
3	932	87.5	198	1	CDNB_CRICTUL	P66439 cricetulus
4	931	87.5	197	1	CDNB_MOUSE	P46414 mus musculus
5	870	81.8	178	1	CDNB_MUSVI	P46529 mustela vis
6	220.5	29.7	316	1	CDNB_HUMAN	P49918 homo sapien
7	212.5	29.7	448	1	CDNB_MOUSE	P49919 mus musculus
8	184.5	17.3	164	1	CDNB_FELCA	O19002 felis silve
9	179.5	16.9	159	1	CDNB_MOUSE	P39689 mus musculus
10	171.5	16.1	164	1	CDNB_HUMAN	P48436 homo sapien
11	98	9.2	1822	1	ZAP3_HUMAN	P49750 homo sapien
12	95	9.0	745	1	ADVA_PAT	O64028 rattus norv
13	96	9.0	1278	1	Y232_HUMAN	O65628 homo sapien
14	95	8.9	399	1	ALX4_MOUSE	O45137 mus musculus
15	94	8.8	735	1	ADDA_MOUSE	O99500 mus musculus
16	93.5	8.8	556	1	HIF1_HUMAN	P46471 homo sapien
17	91.5	8.6	1076	1	IF3A_CAEEL	P23388 caenorhabdi
18	89	8.4	611	1	IF4B_HUMAN	P23588 homo sapien
19	88.5	8.3	382	1	MYF_AVIIM	P31104 avian myelo
20	88	8.3	446	1	CM3A_P15	P64404 sus scrofa
21	88	8.3	1337	1	DEXT_STRUD	P39653 streptococc
22	88	8.3	1461	1	TE18_PRRVP	P11675 pseudorabie
23	87.5	8.2	559	1	ENL_HUMAN	O03111 homo sapien
24	87.5	8.1	1337	1	F327_APT1	P07428 caenorhabdi
25	86	8.1	466	1	IMP2_DROME	P29681 drosophila
26	86	8.1	713	1	YH4A_YEAS1	P39422 homo sapien
27	86	8.1	1276	1	FRG5_HUMAN	P53564 mus musculus
28	86	8.1	1495	1	CUTL1_MOUSE	O99190 arabidopsis
29	85.5	8.0	514	1	WR44_ARATH	P48466 rattus norv
30	85.5	8.0	525	1	MP11_PAT	O54898 rattus norv
31	85.5	8.0	2254	1	CDNA_PAT	O60115 rattus norv
32	85	8.0	467	1	VIR4_HSV11	P80724 bos taurus
33	84.5	7.9	226	1	BASP_BOVIN	

## RESULT 1

ID	CDNB_HUMAN	STANDARD	PRT	198 AA
AC	P46527: Q16307;			
DI	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-MAY-2002 (Rel. 41, Last annotation update)			
DE	Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase inhibitor p27) (p27Kip1).			
DE	Inhibitor p27 (p27Kip1).			
GN	CDKN1B OR Kip1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RI	[1]			
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 28-79 AND 104-152.			
RC	TISSUE=Kidney;			
RA	MEDLINE=94306518; PubMed=8033212;			
PA	Polyak K., Lee M.-H., Erjument-Romage H., Koff A., Roberts J.M.,			
PT	Tempst P., Massague J.;			
PT	"Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a			
PT	potential mediator of extracellular antimitogenic signals."			
RL	Cell 78:59-66(1994).			
RN	[2]			
PP	SEQUENCE FROM N.A.			
PX	MEDLINE=45184144; PubMed=7882109;			
RA	Pietenpol J.A., Bohlender S.K., Sato Y., Papadopoulos N., Liu B.,			
PA	Friedman C., Trask R.J., Roberts J.M., Kinzler K.W., Rowley J.D.;			
RI	"Assignment of the human p27Kip1 gene to 12p13 and its analysis in			
RI	leukemias."			
RL	Cancer Res. 55:1206-1210(1995)			
RN	[3]			
PP	SEQUENCE FROM N.A., AND VARIANTS TP1-15 AND G1Y-109			
PA	Pfister M.T., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,			
PA	Nguyen B.A., Livingston P.T., Paul G.L., Robertson P.D.,			
PA	Schackwitz W.S., Sherwood J.K., Wittek T.A., Nickerson P.A.,			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
PP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 23-106 OF COMPLEX WITH CDK2			
PP	AND CG2A.			
PP	MEDLINE=96300318; PubMed=8684460;			
RA	Pisano A., Jeffrey P.D., Patten A.K., Massague J., Pavletich N.P.;			
PA	"Crystal structure of the p27Kip1 cyclin-dependent-kinase inhibitor			
RI	bound to the cyclin A-Cdk2 complex."			
RL	Nature 392:325-331(1996).			
CC	1-1 FUNCTION: Involved in G1 arrest. May mediate TGF-beta-induced G1			
CC	arrest. Acts to inhibit complexes formed by cyclin E/CDK2,			
CC	cyclin A/CDK2, and cyclin D/CDK4. Interaction with nucleoporin			
CC	NUP50 is required for nuclear import and for degradation of			
CC	phosphorylated p27Kip1 after nuclear import (By similarity)			
CC	1-1 SUBUNIT: Interacts with NUP50 (By similarity).			
CC	1-1 SUBCELLULAR LOCATION: Nuclear.			
CC	1-1 TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED. HIGHEST			
CC	LEVELS IN SKELETAL MUSCLE, LOWEST IN LIVER AND KIDNEY.			
CC	1-1 DOMAIN: A PEPTIDE SEQUENCE CONTAINING ONLY AA 28-79 RETAINS			
CC	SUBSTANTIAL KIP1 CYCLIN A/CDK2 INHIBITORY ACTIVITY			

P23389 bos taurus  
O00515 homo sapien  
Q12600 candida tio  
P74247 synchocyst  
P92969 arabidopsis  
O55112 mus musculus  
P70478 rattus norv  
Q99412 homo sapien  
P20315 saccharomyc  
P40349 ustilago ma  
P97609 rattus norv  
Q11069 caenorhabdi

## ALIGNMENTS





```
CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin
CC NUP50 is required for nuclear import and for degradation of
CC phosphorylated p27Kip1 after nuclear import (By similarity).
CC -!- SUBUNIT: Interacts with NUP50 (by similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
CC
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CC
CC FMRL: U49649; AAA21149.1; -.
CC InterPro: IPR003175; CDI.
CC Pfam: PF02234; Cdi; 1.
CC Cell cycle, Nuclear protein. NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC DOMAIN 153 169
CC SEQUENCE 168 AA: 22349 MW: 28390 PEP: FAF55FA6P9 CPO64.
CC
CC Query Match 87.6%; Score 932; DB 1; Length 198;
CC Best Local Similarity 87.4%; Pred. No. 4.5e-62;
CC Matches 173; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
CC
CC QY 1 MSNVRVNSGSPSLERMDAPQAEHPKPSACPNIFGPDVHEETDLEKHCPODMEASQKWK 60
CC DB 1 MSNVRVNSGSPSLERMDAPQAEHPKPSACPNIFGPDVHEETDLEKHCPODMEASQKWK 60
CC QY 61 NFDQFNHKLPLEGKYEWGEVEKSLPEFYYPKPKGACKVPAQESQVSGSRPAAPLIG 120
CC DB 61 NFDQFNHKLPLEGKYEWGEVEKSLPEFYYPKPKGACKVPAQESQVSGSRPAAPLIG 120
CC QY 121 APANSEDLHLVDPKILPSISQSLAKQWASLKKPAPATDSSSTONKPRANTEENVSDGSPN 180
CC DB 121 SCATSTFPHLVEFMDPITSPALAEQPMKRFPAHQSSQSFANFTFENVSDGSPN 180
CC QY 181 AGSVQTPKKPKGLRRQT 198
CC DB 181 AGSVQTPKKPKGLRRQT 198
CC
CC RESULT 4
CC CNB_MOUSE STANDARD: PPT: 197 AA
CC AC P46414;
CC DT 01-NOV-1995 (Rel. 32, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 15 JUN 2002 (Rel. 41, Last annotation update)
CC DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase
CC inhibitor p27) (p27Kip1).
CC GN CDKN1B.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CC OX NCBI_TaxID=10090;
CC [1]
CC SEQUENCE FROM N.A.
CC RX MEDLINE=94306519; PubMed=8033213;
CC RA Toyoshima H., Hunter T.;
CC RT "p27, a novel inhibitor of cyclin D3 protein kinase activity, is
CC related to p21";
CC RL Cell 78:67-74(1994).
CC [2]
CC SEQUENCE FROM N.A.
CC RC TISSUE=Embryo;
CC RX MEDLINE=94306518; PubMed=8033212;
CC RA Poljak K., Lee M. H., Erdjument-Bromage H., Raff A., Roberts J.M.,
CC RA Tempst P., Massague J.;
CC RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a
CC potential mediator of extracellular antimitogenic signals";
CC RL Cell 78:59-66(1994).
```

```
CC [3]
CC INTERACTION WITH NUP50, AND MUTAGENESIS.
CC STRAIN=GALE/c;
CC MEDLINE=2027197; PubMed=10811608;
CC RA Mueller D., Thieme K., Ruegerlin A., Diekmann A., Eilers M.;
CC RT "Cyclin E-mediated elimination of p27 requires its interaction with
CC the nuclear pore-associated protein MNPAP60.";
CC PL EMBO J 19:3168-3180(2000).
CC -!- FUNCTION: Involved in G1 arrest. May mediate TGF-beta-induced G1
CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,
CC cyclin A-CDK2, and cyclin E1-CDK4. Interaction with nucleoporin
CC NUP50 is required for nuclear import and for degradation of
CC phosphorylated p27Kip1 after nuclear import.
CC -!- SUBUNIT: Interacts with NUP50.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
CC
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CC
CC EMBL: U10440; AAA21149.1; -.
CC FMRL: U09368; AAA20235.1; -.
CC MGD: MGI:104565; Gdnlb.
CC InterPro: IPR003175; Cdi.
CC Pfam: PF02234; Cdi; 1.
CC Cell cycle, Nuclear protein. NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
CC DOMAIN 153 169
CC MUTAGEN 90 90 P-53: LOSS OF INTERACTION WITH NUP50.
CC SEQUENCE 197 AA: 22318 MW: 29140 PEP: FAF55FA6P9 CPO64.
CC
CC Query Match 87.5%; Score 931; DB 1; Length 197;
CC Best Local Similarity 87.4%; Pred. No. 5.4e-62;
CC Matches 172; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
CC
CC QY 1 MSNVRVNSGSPSLERMDAPQAEHPKPSACPNIFGPDVHEETDLEKHCPODMEASQKWK 60
CC DB 1 MSNVRVNSGSPSLERMDAPQAEHPKPSACPNIFGPDVHEETDLEKHCPODMEASQKWK 60
CC QY 61 NFDQFNHKLPLEGKYEWGEVEKSLPEFYYPKPKGACKVPAQESQVSGSRPAAPLIG 120
CC DB 61 NFDQFNHKLPLEGKYEWGEVEKSLPEFYYPKPKGACKVPAQESQVSGSRPAAPLIG 120
CC QY 121 APANSEDLHLVDPKILPSISQSLAKQWASLKKPAPATDSSSTONKPRANTEENVSDGSPN 180
CC DB 121 SCANSEDLHLVDPKILPSISQSLAKQWASLKKPAPATDSSSTONKPRANTEENVSDGSPN 180
CC QY 181 AGSVQTPKKPKGLRRK 196
CC DB 181 AGSVQTPKKPKGLRRQ 196
CC
CC RESULT 5
CC CNB_MOUSE STANDARD: PPT: 178 AA
CC AC P46529;
CC DT 01-NOV-1995 (Rel. 32, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 15 JUN 2002 (Rel. 41, Last annotation update)
CC DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase
CC inhibitor p27) (p27Kip1) (Fragment).
CC GN CDKN1B.
CC OS Mustela vison (American mink).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
CC OC Mustela.
CC OX NCBI_TaxID=9667;
CC [1]
CC SEQUENCE FROM N.A.
CC RP
```











```

QY 126 EPTH-----LVPRKTPSPSOTGLAFQACAPKPKPATRUSSTONKPNRTERVNSG 177
DB 660 ERAHASPLLIQLPLADPEPASASAPGAEVAS-----FATERISPMIDP-----SNG 707
QY 178 SPNAGSVFQTPKKPKPIRPQ 197
DB 708 SFG---KSFKKKKK 719

RESULT 13
Y232_HUMAN          STANDARD;          PPT; 1278 AA.
AC  GQ2628;
DT  01-NOV-1997 (Rel. 45, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DE  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Hypothetical protein KIA0232 (Fragment).
GN  KIA0232.
GS  Homo sapiens (Human).
OC  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC  Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
OX  NCBI_TaxID=9606;
RN  [1]
PP  SEQUENCE FROM N.A.
RA  Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA  Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.
RL  Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN  [2]
PP  SEQUENCE OF 271-1278 FROM N.A.
RA  TISSUE=Rone marrow;
RX  MIMTINF=97191544; PubMed=9039502;
RA  Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA  Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.
RT  "Prediction of the coding sequences of unidentified human genes VI.
RT  The coding sequences of 80 new genes (KIA0201-KIA0280) deduced by
RT  analysis of cDNA clones from cell line KG-1 and brain #;
RL  DNA Res. 3:321-329(1996).
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DB  EMBL: D86985; HAAL3221.2;
DR  Hypothetical protein.
FT  NON_TER 1
SQ  SEQUENCE 1278 AA; 141664 MW; 24070847/APR1440 CRR64;

Query Match          9.0%, Score 96, OR 1, Length 1278;
Best Local Similarity 26.7%, Pred. No. 9, 3;
Matches 47; Conservative 21; Mismatches 62; Indels 46; Gaps 11;

QY 39 PELTRPLPKPQMEASQKWNFPQNIKFLFY-----KYRWLEVKSLFEFFYE 92
DB 11 ETIVPELCKLGLGSLKQEK-----LHKLENSPSPEALSPKAKIV-EMYYEAFPP 64
QY 53 KFKKAA-----KVFALSSQVSSSPFAFLFATANSSEIHILVTKTPSPSSQ 141
DB 64 LSKPPTLTGEIMVNNKSKVTSYSSSSSSSTAPPA-----SDTSS-SPKDENSE 114
QY 142 TSLAECACAPKPPATPSSSTGNKPNKPTFENVSDSTNAGSVETPKKKPKRPQ 157
DB 114 V-TKRSSEV---PTTVKHTOSKSKNKENFSN-----GTIER---KPALYKKQ 157

PESIT 14
ALX4_MOUSE
ID  ALX4_MOUSE
AC  035137;

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```

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE  Homeobox protein aristaless-like 4 (ALX-4).
GN  ALX4.
GS  Mus musculus (Mouse).
OC  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC  Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Mus.
OX  NCBI_TaxID=10090;
RN  [1]
PP  SEQUENCE FROM N.A.
RA  STRAIN=C57BL/6; TISSUE=Embryo;
RX  MEDLINE=98086222; PubMed=9426253;
RA  Qu S., Li J., Wisdom P.;
RT  "Alx-4: cDNA cloning and characterization of a novel paired-type
RT  homeodomain protein.";
RL  Gene 203:217-233(1997).
RN  [2]
PP  VARIANT LST GLN-206.
RA  MEDLINE=98301426; PubMed=9636085;
RA  Co S., Tucker S.C., Ehrlich J.S., LeVorse T.M., Flaherty L.A.,
RA  Wisdom R., Vogt T.F.;
RT  "Mutations in mouse Aristaless-like4 cause Strong's luxoid
RT  polydactyly.";
RL  Development 125:2711-2721(1998).
CC  -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN SKULL AND LIMB
CC  DEVELOPMENT.
CC  -1- SUBUNIT: BINDS DNA.
CC  -1- SUBCELLULAR LOCATION: Nuclear.
CC  -1- TISSUE SPECIFICITY: EXPRESSED IN OSTEOBLASTS. NOT EXPRESSED IN
CC  BRAIN, HEART, INTESTINE, KIDNEY, LIVER, MUSCLE, SPLEEN AND TESTIS.
CC  -1- DEVELOPMENTAL STAGE: EXPRESSED FROM E8.25 AND CONFINED TO
CC  MESENCHYMAL CELLS THROUGHOUT THE EMBRYO DEVELOPMENT. EXPRESSION IS
CC  SEEN AT SEVERAL SITES INCLUDING CRANIOFACIAL REGION, FIRST
CC  BRANCHIAL ARCH AND ANTERIOR ASPECT OF THE LIMB BUD.
CC  -1- DISEASE: DEFECTS IN ALX4 AFFECT THE CAUSE OF STRONG'S LUXOID (LST)
CC  PHENOTYPE. AT HETEROZYGOSITY LST IS CHARACTERIZED BY PREAXIAL
CC  ABNORMALITIES OF THE HINDFEET AND, VERY RARELY, OF THE FOREFEET.
CC  HOMOZYGOES SHOW PREAXIAL POLYDACTYLY OF ALL FOUR LIMBS.
CC  REDUCTIONS AND DUPLICATIONS OF THE RADIUS, ABSENCE OF THE TIBIA,
CC  CRANIOFACIAL DEFECTS, REDUCTION OF THE PHRIS, AND DORSAL ALOPECIA.
CC  -1- SIMILARITY: BELONGS TO THE PAIRED HOMEBOX FAMILY.
CC  -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
CC  -1- SIMILARITY: CONTAINS 1 OAP DOMAIN
CC  -----
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CC  -----
DB  EMBL: AF051455; AAC39943.1;
DR  HSSP; PubMed1; IFJL.
DR  TRANSFAC; T02967;
DB  MGS; MG1:108359; ALX4.
DB  InterPro; IPR003654; Homeo_OAP.
DB  InterPro; IPR001456; Homeobox
DB  Pfam; PF00046; homeobox; 1.
DB  ProDom; PDOM010; Homeobox; 1.
DB  SMART; SM00389; HOX; 1.
DB  PROSITE; PS00027; HOMEBOX_1; 1.
DB  PROSITE; PS50071; HOMEBOX_2; 1.
DB  PROSITE; PS5803; OAP; 1.
DB  Homeobox DNA-binding; Developmental protein, Nuclear protein;
DB  Transcription regulation; Activator; Disease mutation.
FT  DNA_BIND 202..261 HOMEBOX.
FT  DOMAIN 379..392 OAR.
FT  VARIANT 206..206
FT  SEQUENCE 399 AA; 42762 MW; 24E192DACA1D25 CRR64;

```





Genome version 5.1.6  
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OM protein - protein search, using sw mode!

Run on: May 30, 2003, 08:53:57 : Search time 34.5449 seconds  
(without alignments)  
1181.337 Million cell updates/seq

Title: US-09-865-018b-2  
Perfect score: 1004  
Sequence: 1 MSNVRVNSGSPSLERMDARQ

Scoring table: BLOSUM62 PNA:SVPLTKKPKLFFKQ 198  
Gap: 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SPTREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mimic:\*
- 8: sp\_organella:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp Vertebrate:\*
- 14: sp\_undefined:\*
- 15: sp\_virus:\*
- 16: sp\_bacterioph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1058	99.4	198	4 Q9NYG6	Q9NYG6 homo sapien
2	1057	99.3	198	4 Q9NSK6	Q9NSK6 homo sapien
3	1054	99.1	198	4 Q96TE0	Q96TE0 homo sapien
4	976	91.7	198	6 Q9BDC3	Q9BDC3 sus scrofa
5	924	86.8	197	11 Q08769	Q08769 rattus norv
6	919	86.4	197	11 Q35792	Q35792 rattus norv
7	852	80.1	158	4 Q43806	Q43806 homo sapien
8	762	71.6	172	6 Q9BEA5	Q9BEA5 sus scrofa
9	347	32.6	179	13 Q90XK4	Q90XK4 brachydanio
10	218	20.5	210	13 Q91K63	Q91K63 xenopus lae
11	214	20.1	42	4 Q90HE0	Q90HE0 homo sapien
12	214	20.1	259	13 Q91K46	Q91K46 xenopus lae
13	211	19.8	335	11 Q91V06	Q91V06 mus musculus
14	191	18.0	164	11 Q64X15	Q64X15 rattus norv
15	190	17.9	42	11 Q9QX80	Q9QX80 rattus norv
16	172	15.2	164	4 Q64X11	Q64X11 homo sapien

17	170.5	16.0	181	4	Q14010	Q14010 homo sapien
18	151.5	14.2	258	5	Q22198	Q22198 caenorhabdi
19	141	13.3	259	5	Q900K5	Q900K5 caenorhabdi
20	125	11.7	184	5	Q22197	Q22197 caenorhabdi
21	110.5	10.4	253	5	Q8WQ22	Q8WQ22 drosophila
22	102	9.6	518	5	Q960X2	Q960X2 drosophila
23	102	9.6	1465	5	Q9WMD0	Q9WMD0 drosophila
24	102	9.6	1645	5	Q8WSS9	Q8WSS9 drosophila
25	100	9.4	191	10	Q04154	Q04154 arabidopsis
26	100	9.4	191	10	Q82899	Q82899 arabidopsis
27	100	9.4	341	10	Q88RQ3	Q88RQ3 arabidopsis
28	98.5	9.3	245	5	Q94536	Q94536 drosophila
29	98.5	9.3	755	4	Q43714	Q43714 homo sapien
30	98.5	9.3	883	4	Q94MNR	Q94MNR homo sapien
31	98	9.2	795	5	Q95022	Q95022 toxoplasma
32	97	9.1	255	5	Q91654	Q91654 drosophila
33	96.5	9.1	245	5	Q91658	Q91658 drosophila
34	95	8.9	393	10	Q858M4	Q858M4 arabidopsis
35	95	8.9	1173	11	Q62018	Q62018 mus musculus
36	94.5	8.9	1008	10	Q9FNE4	Q9FNE4 arabidopsis
37	94	8.8	246	3	Q03973	Q03973 saccharomyc
38	94	8.8	637	11	Q8R149	Q8R149 mus musculus
39	94	8.8	861	5	Q21186	Q21186 caenorhabdi
40	94	8.8	3664	4	Q9Y556	Q9Y556 homo sapien
41	94	8.8	3664	4	Q96T58	Q96T58 homo sapien
42	93.5	8.8	500	11	Q922K1	Q922K1 mus musculus
43	93.5	8.8	798	10	Q94DW7	Q94DW7 oryza sativ
44	93.5	8.8	1307	11	Q88974	Q88974 mus musculus
45	93.5	8.8	1323	4	Q90KE0	Q90KE0 homo sapien

## ALIGNMENTS

### RESULT 1

ID	Q9NYG6	PRELIMINARY:	PRT:	198 AA.
AC	Q9NYG6:			
DT	01-OCT-2000 (Tremblrel. 15, Created)			
DI	01-OCT-2000 (Tremblrel. 15, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	Cyclin-dependent kinase inhibitor p27kip1.			
OS	Homo sapiens (Human).			
OC	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi:			
OC	Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.			
OX	NCRL_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
KC	TISSUE=HEPATOMA;			
RA	Li J, Wang W-L, Yang X-K, Yu X-X;			
PT	*Homo sapiens cyclin dependent kinase inhibitor p27kip1 cDNA.*;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF247551; AAF69497.1;			
DR	InterPro: IPR003175; CDI.			
DR	Pfam: PF02234; CDI; 1.			
KW	Kinase.			
SQ	SEQUENCE 198 AA: 22099 MW: 407058901CDFAA CRC64:			

Query Match	99.4%	Score 1058:	DB 4:	Length 198:
Best local Similarity	99.5%	Prod No	6,5e-82:	
Matches 197:	Conservative	0:	Mismatches 1:	Indels 0:
Gaps	0:			

Cy	1	MSNVRVNSGSPSLERMDARQAEHPKPSATPNLPGVDHEELTPDLKHCDFEASQRKW	60
Db	1	MSNVRVNSGSPSLERMDARQAEHPKPSACKNLPGVDHEELTKDLKHCDFEASQRKW	60
Cy	61	NFQFQNHKFLGKYEWEKESLPPFYFPPPPKAGAKVFAEFSSVSSSPFAAFLLG	120
Db	61	NFQFQNHKFLGKYEWEKESLPPFYFPPPPKAGAKVFAEFSSVSSSPFAAFLLG	120
Cy	121	APANSFTHLVPEKTIQSPSSQDGLAPFAAIFPKPPAIISSSTONKFPANPEENVSQSPN	180
Db	121	APANSFTHLVPEKTIQSPSSQDGLAPFAAIFPKPPAIISSSTONKFPANPEENVSQSPN	180





[illegible]

```

DE Cyclin dependent kinase inhibitor p27 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Waltrney D., Loda M.;
RT "Homo sapiens cyclin-dependent kinase inhibitor p27 intron. ";
PL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF213700; AAF21068.1; -
KW Kinase.
FT NON_TER 1
FT NON_TER 42
FT NON_TER 42
SQ SEQUENCE 42 AA: 4461 MW: 92637498.2A590CD9 CRC64;

Query Match 20.1%, Score 214; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 LAFCACGIPKPPATPDSSQNKPRANPTFFNVSDSPNAGSVE 185
Db 1 LAEQACGIPKPPATPDSSQNKPRANPTFFNVSDSPNAGSVE 42

RESULT 12
Q91646 PRELIMINARY; PRT; 209 AA
AC Q91646;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclin-dependent kinase inhibitor p28.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
OC Amphibia; Batrachia, Anura, Mesokotrichia, Pipiloidea; Pipiloidea;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Shou W., Dunphy W.G.;
RT Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases
DR EMBL: U38844; AAC5975.1; -
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KW Kinase.
SQ SEQUENCE 209 AA: 23475 MW: 49941427.400; CRC64,

Query Match 20.1%, Score 214; DB 13; Length 209;
Best Local Similarity 27.9%; Pred. No. 1.4e-10;
Matches 56; Conservative 38; Mismatches 79; Indels 28; Gaps 6;

QY 14 BRMDARQEHKPS-----ACRNLFQFVDHEELTRDLKHKCRDMBEASQKKNWFQNH 67
Db 10 FEMISAPAVLDFLNGTGGWAKRNLPAPLHDMKPSSELKPKLKLQASDQPMWNPDPETG 69
QY 68 KPIFGKYPQWKEGSLPEFYEPYPPPKKACKPAGESQIVSSRFAAPLIGAPANSEJ 127
Db 70 IFLKJFCWEPEVSKOMPSFSONPSTAAATPSPKQQLQLLLVSPQLPEPEAPVITV 128
QY 128 THLVDFKTFDSQTLGAAGAGIKKFAIGSSQNKRRANKE-----TEENVSD 176
Db 129 NVNPNPCAKENAEK1--VKRGGVK-GRKASANTSTQRRKREITPILDFPKKKKILS 185
QY 177 GSNAGS-----VEQTPKK 190

```

```

Db 186 AKPLATKGAHLGLCPLEUTPRK 206

RESULT 13
Q91V06 PRELIMINARY; PPT; 335 AA
AC Q91V06;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cyclin dependent kinase inhibitor 1C (p57Kip2 protein) (P57).
GN CDKN1C OR P57KIP2.
OS Mus musculus domesticus (western European house mouse), and
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae; Murinae; Mus.
OX NCBI_TaxID 10092; 10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Musculus domesticus; STRAIN=129 SV;
RX MEDLINE-20519229; PubMed-11063728;
RA Engemann S., Stroedter M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
RT implications for a novel imprinting centre and extended imprinting. ";
PL Hum Mol Genet 9:2691-2706(2000)
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Musculus domesticus; STRAIN=129 SV;
RA Engemann S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=129/SV;
RX MEDLINE-20314712; PubMed-10545601;
RA John P.M., Hodges M., Little P., Barton S., Surani M.A.;
RT "A human p57KIP2 transgene is not activated by passage through the
RT maternal mouse germline. ";
PL Hum. Mol. Genet. 8:2211-2219(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; TISSUE=BREAST TUMOR;
RA Strausberg R.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases
DR PMBL: AJ276505; AAC16402.1; -
DR EMBL: AF160190; AAF00983.1; -
DR EMBL: BC005412; AAH05412.1; -
DR MGD: MGI_104564; Cdkn1c
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KW Kinase.
SQ SEQUENCE 335 AA: 35903 MW: 55040675287FEB3F CRC64;

Query Match 19.8%, Score 211; DB 11; Length 335;
Best Local Similarity 30.9%; Pred. No. 4.5e-10;
Matches 65; Conservative 48; Mismatches 60; Indels 46; Gaps 8;

QY 25 KPSACRNLFQFVDHEELTRDLKHKCRDMBEASQKKNWFQNHKPLE--GKVEQVEK 82
Db 15 RSSACRSIFQFVDHEELTRDLKHKCRDMBEASQKKNWFQNDVPLRGFGRLOWMEVDSE 74
QY 83 SLPEFYPP-----PPPKKACKV-----PAGESQIVSSRFAAPLIGAPANS 125
Db 75 SVIAPFYPPVQVSGKCHQLQPPPPHVAVAIIPSSCHPAGKAPGIGLEAPKQPPSAPASA 133
QY 126 FTHLVTPKTFPSQTLGAELWAGIKKPKPATIDSS-----PLNKKRANKTEENVSDSP 179
Db 134 -----VVAEPPTPA-----TPAPASDLISDP1PEVTLVAISDFIDP1DAMP 176
QY 180 NAGS-----VEQTPKK 190
Db 177 DVATRDGEQVPEQ 190

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 08:52:12 : Search time 14.7158 Seconds  
(without alignments)  
606.682 Million cell updates/sec

Title: US-09-865-018b-2\_Nov\_22\_98

Perfect score: 383

Sequence: 1 FHPKPSACPMLPGVDHREI.....PLETKYFQWQFVKGSLPEFY 67

Scoring table: BLOSUM62

Gap: 10.0, Gap-ext: 0.5

Searched: 908470 seqs 13250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*  
1: /SID2/qcdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SID2/qcdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SID2/qcdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SID2/qcdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SID2/qcdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
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10: /SID2/qcdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SID2/qcdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SID2/qcdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SID2/qcdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SID2/qcdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
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18: /SID2/qcdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SID2/qcdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SID2/qcdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SID2/qcdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SID2/qcdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SID2/qcdata/geneseq/geneseq-emb1/AA2002.DAT.\*

pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	383	100.0	167	20	AAW95101
2	383	100.0	177	21	AAW97530
3	383	100.0	177	21	AAW96045
4	383	100.0	177	21	AAW96072
5	383	100.0	194	20	AAW94940
6	383	100.0	194	16	AAW94944
7	383	100.0	198	17	AAW92709
8	383	100.0	198	19	AAW92717
9	383	100.0	198	19	AAW46888
10	383	100.0	198	20	AAW00768

11	383	100.0	198	21	AAW97523	Human p27 protein
12	383	100.0	198	21	AAW96052	Human cyclin depen
13	383	100.0	198	21	AAW96066	Human cyclin depen
14	383	100.0	198	21	AAW70307	Human mutant cycli
15	383	100.0	198	21	AAW44400	Human p27(Kip1) ki
16	383	100.0	198	22	AAW84649	Amino acid sequenc
17	383	100.0	198	22	AAW48309	Human p27 protein.
18	383	100.0	198	23	AAW47880	p27-Kip1. Homo sa
19	383	100.0	334	20	AAW95103	Truncated p27/p16
20	383	100.0	334	21	AAW97532	Human W8 protein s
21	383	100.0	334	21	AAW96047	Antiproliferative
22	383	100.0	334	21	AAW96074	Angiogenesis inhib
23	383	100.0	348	20	AAW95104	Truncated p27/p16
24	383	100.0	348	21	AAW97531	Human W7 protein s
25	383	100.0	348	21	AAW96046	Antiproliferative
26	383	100.0	348	21	AAW96073	Angiogenesis inhib
27	383	100.0	365	18	AAW23536	CDK inhibitory fus
28	383	100.0	365	20	AAW95107	Human p16p27 fusio
29	383	100.0	365	20	AAW95096	Human p16p27 fusio
30	383	100.0	365	21	AAW97527	Human W4 protein s
31	383	100.0	365	21	AAW97529	Human W6 protein s
32	383	100.0	365	21	AAW96042	Antiproliferative
33	383	100.0	365	21	AAW96044	Antiproliferative
34	383	100.0	365	21	AAW96069	Angiogenesis inhib
35	383	100.0	365	21	AAW96071	Angiogenesis inhib
36	383	100.0	380	18	AAW23535	CDK inhibitory fus
37	383	100.0	380	20	AAW94095	Human p16(GS)p27 f
38	383	100.0	380	21	AAW97528	Human W5 protein s
39	383	100.0	380	21	AAW96043	Antiproliferative
40	383	100.0	380	21	AAW96070	Angiogenesis inhib
41	383	100.0	391	18	AAW23534	CDK inhibitory fus
42	383	100.0	391	20	AAW95094	Human p27-p16 tusi
43	383	100.0	391	21	AAW97526	Human W3 protein s
44	383	100.0	391	21	AAW96041	Antiproliferative
45	383	100.0	391	21	AAW96068	Angiogenesis inhib

#### ALIGNMENTS

##### RESULT 1

AAW95101 standard. Protein: 167 AA.

XX AAW95101:

XX 25-MAY-1999 (first entry)

XX Truncated p27 protein.

XX Cyclic-dependent kinase, CDK, cdk-cyclin complex, inhibitory, restenosis;  
XX cdk binding motif, end-theletelastase, fusio protein, thepentin, acne,  
XX intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
XX smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
XX cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
XX tumor; inflammation; neurodegeneration; periodontal; spermatogenesis;  
XX tachycardia; human, p27; truncated.

XX Homo sapiens.

XX W0906540-A2.

XX 11-FEB-1999.

XX 29-JUL-1998. 98W00515759.

XX 29-JUL-1997. 97US 0902572.

XX (MITO-) MITOTIX INC.

XX Beach DR, Gyuris J, Lamphere L,

XX WPI; 1999-153770/13.





PI Novel recombinant lentivirus for inhibiting proliferation of smooth  
 PT muscle cells in e.g. restenosis, is replication deficient and comprises  
 PT a transgene encoding a cyclin dependent kinase inhibitor

XX Example 1, Page 109-110, 126pp, English.

XX The present sequence is that of truncated human p27 protein in  
 CC which the first 12 N-terminal and the final 21 C-terminal amino  
 CC acids of full-length p27 (see AAY96052) are deleted to remove a CDK  
 CC consensus phosphorylation site at amino acids 187-190, a potential  
 CC phosphorylation site for proline-directed kinases at amino acids  
 CC 178-181 and a weak CDK phosphorylation site at amino acids 10-13.  
 CC p27 is a cyclin dependent kinase inhibitor (CKI). A claimed  
 CC method for inhibiting smooth muscle cell hyperproliferation involves  
 CC transducing smooth muscle cells with a replication-deficient  
 CC recombinant adenovirus that lacks a functional E1 region and a  
 CC functional E4 region, and comprises a transgene encoding a CKI.  
 CC The CKI is an INK4 family protein such as human p16, a CIP/KIP  
 CC family protein such as p27, active fragments of these, e.g.  
 CC p27(12-178aa), or fusion proteins comprising active fragments of)  
 CC an INK4 family protein and a CIP/KIP family protein (see AAY96046 and  
 CC AAY96049). The method is used to inhibit mammalian smooth muscle  
 CC cell hyperproliferation induced by injury caused by angioplasty,  
 CC stent placement or vein engraftment. It is useful for treating  
 CC vascular pathologies, e.g. restenosis. Also claimed are recombinant  
 CC lentiviruses encoding CKIs. Use of truncated p27 was designed to  
 CC increase the protein's half-life and to eliminate potential  
 CC phosphorylation sites involved in the negative regulation of CKI  
 CC activity.

XX Sequence 177 AA:

Query Match. 100.0%; Score 383; Db 21; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 8, 2e-41;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHKPSACRNLFQGVVDEELIKPFRKCHIMFASQPKWNFFQNHKPIFGKYEWQVEVK 50  
 DB 22 EHKPSACRNLFQGVVDEELIKPFRKCHIMFASQPKWNFFQNHKPIFGKYEWQVEVK 81  
 QY 61 GSLPEFY 67  
 DB 82 GSLPEFY 88

RESULT 4

AA96072  
 ID AAY96072 standard; Protein: 177 AA.

AC AAY96072;

XX 05-DEC-2000 (first entry)

XX Human cyclin dependent kinase inhibitor p27(12-178).

XX Cyclin dependent kinase inhibitor, CKI, CIP, KIP, human, p27,  
 KW angiogenesis inhibitor, neoplasia, rheumatoid arthritis;  
 KW endometriosis, psoriasis, vascular retinopathy, cytostatic;  
 KW antirheumatic; antirheumatic; gynaecological; antipsoriatic;  
 KW antiproliferative; gene therapy; mutant; mutagen.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FI Peptide 1..11

FI /label= Haemagglutinin-epitope

FI Protein 12..177

FI /label= p27(12-178)

XX W02000052159-A1.

XX 08-SEP-2000.

XX 28-FEB-2000; 2000W0-0504970.

XX 01-MAP-1999; 400S-0122974.

XX 06-MAY-1999; 99US-0163682

XX 09-DEC-1999; 99US-0457646.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX Patel S, McArthur J, Gyuris J;

XX WPI: 2000-565501/52.

XX N-PSDB; AAA5057.

XX Inhibiting angiogenesis and treating angiogenesis-associated  
 PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
 PT cell with a recombinant virus having a transgene encoding a cyclin  
 PT dependent kinase inhibitor

XX Example 1; Page 117-118; 138pp; English.

XX The present sequence is that of a truncated human p27 protein in  
 CC which the first 12 N-terminal and the final 21 C-terminal amino  
 CC acids of full-length p27 (see AAY96066) are deleted to remove a CDK  
 CC consensus phosphorylation site at amino acids 187-190, a potential  
 CC phosphorylation site for proline-directed kinases at amino acids  
 CC 178-181 and a weak CDK phosphorylation site at amino acids 10-13.  
 CC p27 is a cyclin dependent kinase inhibitor (CKI) that inhibits  
 CC angiogenesis. A claimed method for inhibiting angiogenesis  
 CC involves transducing an epithelial cell with a transgene encoding  
 CC (internalizable, secretable) CKI. The delivery system for the  
 CC transgene may be a liposome or a recombinant virus. The CKI is  
 CC a protein of the CIP/KIP family such as p27, a protein of the  
 CC INK4 family such as p16, active fragments of these proteins (e.g.  
 CC amino acids 25-93 or 12-178 of human p27), or a fusion protein  
 CC comprising 2 CKI proteins such as (truncated) p27 and p16 (see  
 CC AAY96068-80). The method is used to treat conditions associated with  
 CC angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis,  
 CC psoriasis and vascular retinopathy (claimed). Alternatively, the  
 CC transgene is delivered to an auxiliary cell, and is expressed by  
 CC that cell such that the CKI is released into the blood and  
 CC contacts the target epithelial cell. Use of truncated p27 was  
 CC designed to increase the protein's half-life and to eliminate  
 CC potential phosphorylation sites involved in the negative  
 CC regulation of CKI activity.

XX Sequence 177 AA;

Query Match. 100.0%; Score 383; DB 21; Length 177;

Best Local Similarity 100.0%; Pred. No. 8, 2e-41;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 EHKPSACRNLFQGVVDEELIKPFRKCHIMFASQPKWNFFQNHKPIFGKYEWQVEVK 60

DB 22 EHKPSACRNLFQGVVDEELIKPFRKCHIMFASQPKWNFFQNHKPIFGKYEWQVEVK 81

QY 61 GSLPEFY 67

DB 82 GSLPEFY 88

RESULT 5

AA94930

ID AAY94930 standard; Protein: 194 AA.

XX AC AAY94930;

XX 11-MAY-1999 (first entry)

XX Amino acid sequence of p27 protein.

XX Vascular proliferative disease, p27 protein; fusion protein; restenosis;



KW p27 protein; Kipl; cyclin E; Cdk2; cell proliferation; ulcer;  
 KW cancer; hyperplasia; diagnosis; therapy.

XX Homo sapiens.

XX W09602140-A1.

XX 01-FEB-1996.

XX 07-JUN-1995; 95WO-US07361

XX 15-MAR-1994; 94US-0275483

XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.

XX (SLAK ) SUGAN KETTERING INST CANCER RES.

XX Koff A, Massague J, Polyak K, Roberts JM;

XX WP1; 1996-105554/11.

XX N-PSDB; AAL16336.

XX p27, an inhibitor of cyclin E-Cdk2 complex activation, and agents  
 PT which enhance and inhibit its activity, useful for treating  
 PT hyperproliferative and hyperproliferative disorders.

XX Disclosure; Fig 15a-b; 129pp; English.

XX A cDNA clone (AAL16336) derived from human kidney codes for a 27  
 CC kDa protein, p27 Kipl (AAR92709), that is capable of binding to  
 CC and inhibiting the activation of a cyclin E-Cdk2 complex. Human  
 CC Kipl shows a high degree of homology to mink (AAR92707) and mouse  
 CC (AAR92708) Kipl proteins, and the N terminal half of the protein shows  
 CC significant homology to Cipl/WAF1. Kipl shows cdk inhibitory  
 CC activity and prevents cdk2 activation. Overexpression inhibits  
 CC cell entry to the S phase. Kipl can be produced by expression of  
 CC the cDNA clone in cultured cells. It can be used in vitro  
 CC assays to screen agents that affect p27 activity, and in methods  
 CC for the diagnosis and treatment of hyperproliferative disorders,  
 CC e.g. ulcer, and hyperproliferative disorders, e.g. cancer and  
 CC hyperplasia.

XX Sequence 198 AA;

Query Match 100.0%; Score 383; DB 17; Length 198;

Best Local Similarity 100.0%; Pred No. 9.4e-41;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 EHKPSACPNLFGPVVGHHELTPILEKHCPTMEFASQPKWNFDQNHKPLEGKYWQVEVK 60

DB 22 EHKPSACPNLFGPVVGHHELTPILEKHCPTMEFASQPKWNFDQNHKPLEGKYWQVEVK 81

QY 61 GSLPEFY 67

DB 82 GSLPEFY 88

RESULT 8

AAW29717

ID AAW29717 standard; Protein: 198 AA.

XX AAW29717;

XX 27-OCT-1998 (first entry)

DE 27 kDa protein inhibiting activation of cyclin E-Cdk2 complex.

XX 27 kDa protein; p27; Kipl; inhibits activation; cancer; breast carcinoma;

KW cyclin E-cyclin dependent kinase2 complex; hyperproliferative disease;

XX recurrence; treatment; human.

XX Homo sapiens.

XX W09834121-A2.

XX 06-AUG-1998.

XX 04-FEB-1998; 98WO-US01893.

XX 03-FEB-1997; 97US-0794002.

XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.

XX Porter PL, Roberts JM;

XX WP1; 1998-447612/37.

XX N-PSDB; AAV47517.

XX Assays for protein p27 inhibiting activation of cyclin E-cdk2  
 PT complex - useful for, e.g. diagnosis and prognosis of cancer,  
 PT especially breast carcinoma

XX Claim 18, Fig 15B; 105pp; English.

XX The present sequence represents a 27 kDa protein (p27 or Kipl) which  
 CC inhibits the activation of a cyclin E-cyclin dependent kinase2 (cdk2)  
 CC complex. A reduced relative level of Kipl is indicative of a  
 CC hyperproliferative disease (particularly cancer, especially breast  
 CC carcinoma) and also is prognostic for increased risk of death and/or  
 CC recurrence of cancer (and may be used to determine suitable treatments).  
 CC Agents that affect the activity of Kipl can be used to treat  
 CC hyperproliferative conditions, e.g. to stimulate tissue or organ repair  
 CC or to establish cell cultures.

XX Sequence 198 AA;

Query Match 100.0%; Score 383; DB 19; Length 198;

Best Local Similarity 100.0%; Pred No. 9.4e-41;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHKPSACPNLFGPVVGHHELTPILEKHCPTMEFASQPKWNFDQNHKPLEGKYWQVEVK 60

DB 22 EHKPSACPNLFGPVVGHHELTPILEKHCPTMEFASQPKWNFDQNHKPLEGKYWQVEVK 81

QY 61 GSLPEFY 67

DB 82 GSLPEFY 88

RESULT 9

AAW46888

ID AAW46888 standard; Protein: 198 AA.

XX AAW46888;

XX 15-JUN-1998 (first entry)

XX Amino acid sequence of the p27Kipl protein.

XX E7 oncoprotein; proliferative state; HPV; kinase activity;

KW cyclin/cyclin-dependent kinase; p21Cip1; interaction; inactivation;

KW cyclin/cyclin-dependent kinase inhibitor.

XX Homo sapiens.

XX US5736318-A.

XX 07-APR-1998.

XX 17-MAR-1995; 95US-0406248.

XX 17-MAR-1995; 95US-0406248.

XX (HARD ) HARVARD COLLEGE.

XX (HARD ) UNIV HAPVARD

XX Jones DL, Munger K;



```

DR WP1: 2000-587315/55
DR N-PSDB: AAA96020
XX Protein and nucleic acid compositions for preventing and treating
PT neoplasias (particularly cancer); comprises a novel chimeric cyclin
PT dependent kinase inhibitor and adenovirus E4 protein -
XX
XX Example 1: Page 122; 126pp; English.
XX
CC This sequence represents the human p27 protein.
CC The invention relates to a protein composition comprising a novel
CC purified chimeric cyclin dependent kinase inhibitor (CDKi) and a
CC purified adenovirus E4 protein. The compositions comprising the protein,
CC or the DNA encoding it are useful for treating neoplasias in animals. The
CC compositions also find use in assays to eliminate a specific
CC sub-population of cultured cells, to determine the susceptibility of
CC neoplastic cells to treatment with the compositions and also in assays to
CC synchronise cell growth in cultured cells.
XX
XX Sequence 198 AA:
SQ
SQ Query Match 100.0%; Score 383; DB 21; Length 198;
Best Local Similarity 100.0%; Pred No. 4 4e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EHKPSACNLPFGPVDFHEELTRQIFKHCPCDMFEASQPKWNFDONHKPLEGKYEWQVEVK 60
Db 22 EHKPSACNLPFGPVDFHEELTRQIFKHCPCDMFEASQPKWNFDONHKPLEGKYEWQVEVK 81
QY 61 GSLPEFY 67
Db 82 GSLPEFY 88
XX
XX RESULT 12
XX AAY96052
ID AAY96052 standard; Protein: 198 AA.
XX AC AAY96052,
XX 05-DEC-2000 (first entry)
XX Human cyclin dependent kinase inhibitor p27
XX Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; human; p27;
KW smooth muscle cell; restenosis; vasotrophic; antiproliferative;
KW gene therapy.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 25..93 /note= "CDK inhibitory domain"
XX Domain 144..194 /note= "QT domain"
XX Peptide 152..166 /note= "nuclear localisation signal"
XX Modified-site 10..13 /note= "O-phosphorylated; weak CDK phosphorylation site"
XX Modified-site 178..181 /note= "O-phosphorylated; phosphorylation site for proline-directed kinases"
XX Modified-site 187..190 /note= "O-phosphorylated; CDK phosphorylation consensus site"
XX
XX W02000052159-A1.
XX 08-SEP-2000.
XX 28-FEB-2000; 2000W0 US04971.
XX

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DR 01 MAR 1999; 9905 0122974.
DR 05-NOV-1999; 9905-0163682.
DR 04-DEC-1999; 9905-0457568.
XX (CELL-) CELL GENESYS INC.
XX (MITO-) MITOTIX INC.
XX
XX McArthur J, Gyuris J, Finer M;
XX WP1: 2000-584183/56
DR N-PSDB: AAA50499.
XX
XX Novel recombinant activators for inhibiting proliferation of smooth
PT muscle cells in a restenosis, is replication deficient and comprises
PT a transgene encoding a cyclin dependent kinase inhibitor -
XX
XX Example 1: Page 119-120; 126pp; English.
XX
XX The present sequence is that of human p27, a cyclin dependent
XX kinase inhibitor (CDKi) that inhibits smooth muscle cell
XX proliferation. A claimed method for inhibiting smooth muscle cell
XX hyperproliferation involves transducing smooth muscle cells with a
XX replication-deficient recombinant adenovirus that lacks a functional
XX E1 region and a functional E4 region, and comprises a transgene
XX encoding a CDKi. The CDKi is selected from an INK4 family protein
XX such as human p16, a CIP/KIP family protein such as p27, active
XX fragments of these, or fusion proteins comprising (active fragments
XX of) an INK4 family protein and a CIP/KIP family protein (see AAY96046
XX and AAY96049). The method is used to inhibit mammalian smooth muscle
XX cell hyperproliferation induced by injury caused by angioplasty,
XX stent placement or vein engraftment. It is useful for treating
XX vascular pathologies, e.g. restenosis. Also claimed are recombinant
XX lentiviruses encoding CDKis.
XX
XX Sequence 198 AA:
SQ
SQ Query Match 100.0%; Score 383; DB 21; Length 198;
Best Local Similarity 100.0%; Pred No. 4 4e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EHKPSACNLPFGPVDFHEELTRQIFKHCPCDMFEASQPKWNFDONHKPLEGKYEWQVEVK 60
Db 22 EHKPSACNLPFGPVDFHEELTRQIFKHCPCDMFEASQPKWNFDONHKPLEGKYEWQVEVK 81
QY 61 GSLPEFY 67
Db 82 GSLPEFY 88
XX
XX RESULT 13
XX AAY96066
ID AAY96066 standard; Protein: 198 AA.
XX AC AAY96066;
XX 05-DEC-2000 (first entry)
XX Human cyclin dependent kinase inhibitor p27.
XX Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; human; p27;
KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;
KW endometriosis, psoriasis, vascular retinopathy, cytostatic,
KW antiarthritic, antirheumatic, gynaecological, antipsoriatic,
KW antiproliferative; gene therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 25..93 /note= "CDK inhibitory domain"
XX Domain 144..194 /note= "QT domain"
XX Peptide 152..166

```



XX p27(Kip1) kinase inhibitor protein, FKBP 12, p27(Kip1), FKBP-12 complex,  
 KW cytosolic drug-binding protein; yeast two hybrid assay system,  
 KW cell differentiation; apoptosis; neurodegeneration; tumorigenicity;  
 KW cell proliferation related disorder; atherosclerosis; autoimmune disease;  
 KW transplant rejection; inflammation; allergy; cancer; viral infection;  
 KW membranous nephropathy; CDK; cyclin-dependent kinase.

Homosapiens.

Key

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1005-2326-01

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NOTES

(CURR) (CURR)

Nandabalan K.,

WP1; 2000-1165

diagnosis of,

Claim 1; Fig 1

The present se

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Journal of

### try Match

ches 67: 60

1 ЕНРКА

22 CHIKR









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: TITLE OF INVENTION: METHOD FOR TREATING VASCULAR PROLIFERATIVE DISEASES
: FILE REFERENCE: 8642/4
: CURRENT APPLICATION NUMBER: US/08/997,333A
: CURRENT FILING DATE: 1998-07-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 198
: TYPE: PRT
: ORGANISM: Homo sapiens
US-08-897-333A-2

Query Match 100.0% Score 383; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.5e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFQGVDPHEFTLDLKKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 60
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DB 22 EHPKPSACNLFQGVDPHEFTLDLKKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67
|||||
DB 82 GSLPEFY 88

RESULT 6
US-09-240-906-6
: Sequence 6, Application US/09240906
: Patent No. 6245965
: GENERAL INFORMATION:
: APPLICANT: ROUSSEL, MARTINE F.
: APPLICANT: SWEYNE, RICHARD
: APPLICANT: ZINDY, FREDERIQUE
: APPLICANT: CUNNINGHAM, JUSTINE
: TITLE OF INVENTION: CELLS THAT LACK P19INK4D AND P27KIP1 ACTIVITY AND
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 1340-1-025
: CURRENT APPLICATION NUMBER: US/09/240-906
: CURRENT FILING DATE: 1999-01-29
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 198
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-240-906-6

Query Match 100.0% Score 383; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.5e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFQGVDPHEFTLDLKKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 60
|||||
DB 22 EHPKPSACNLFQGVDPHEFTLDLKKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67
|||||
DB 82 GSLPEFY 88

RESULT 7
US-08-794-002-2
: Sequence 2, Application US/08794002
: Patent No. 6316208
: GENERAL INFORMATION:
: APPLICANT: Roberts, James M.
: APPLICANT: Porter, Peggy L.
: TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHODS FOR ITS
: TITLE OF INVENTION: PRODUCTION AND USE
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FOLEY, HOAG & ELLIOT LLP

```

```

: STREET: One Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109-2170
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/794,002
: FILING DATE: 03-FEB-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Vincent, Matthew P.
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MIV-079,03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: #17-842-1000
: TELEFAX: 617-832-7000
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 198 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-794-002-2

Query Match 100.0% Score 383; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.5e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFQGVDPHEFTLDLKKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 60
|||||
DB 22 EHPKPSACNLFQGVDPHEFTLDLKKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67
|||||
DB 82 GSLPEFY 88

RESULT 8
US-09-457-568-26
: Sequence 26, Application US/09457568
: Patent No. 6413943
: GENERAL INFORMATION:
: APPLICANT: McArthur, James G
: APPLICANT: Gyuris, Jeno
: APPLICANT: Finer, Mitchell H
: TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
: TITLE OF INVENTION: Smooth Muscle Cells
: FILE REFERENCE: 106482-691
: CURRENT APPLICATION NUMBER: US/09/457,568
: CURRENT FILING DATE: 1999-12-09
: EARLIER APPLICATION NUMBER: 60/122,974
: EARLIER FILING DATE: 1999-03-01
: EARLIER APPLICATION NUMBER: 60/163,682
: EARLIER FILING DATE: 1999-11-05
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 26
: LENGTH: 198
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-457-568-26

Query Match 100.0% Score 383; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.5e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFQGVDPHEFTLDLKKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 60
|||||

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Query Match 100.0%; Score 383; DB 4; Length 342;  
Best Local Similarity 100.0%; Pred. No. 3 1e-41;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFGPVDPVDEELTRDLEKHCRCRMEASQKKNWDFQNHKPLEGKYEWQVEVK 80  
DB 22 EHPKPSACNLFGPVDPVDEELTRDLEKHCRCRMEASQKKNWDFQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67  
DB 82 GSLPEFY 88

RESULT 13  
US-09-457-568-14  
; Sequence 14, Application US/09457646  
; Patent No. 6420345  
; GENERAL INFORMATION:  
; APPLICANT: Patel, Salil D  
; APPLICANT: McArthur, James G  
; APPLICANT: Gyuris, Jeno  
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of  
; TITLE OF INVENTION: Smooth Muscle Cells  
; FILE REFERENCE: 106482.287  
; CURRENT APPLICATION NUMBER: US/09/457,646  
; CURRENT FILING DATE: 1999-12-09  
; EARLIER APPLICATION NUMBER: 60/122,974  
; EARLIER FILING DATE: 1999-03-01  
; EARLIER APPLICATION NUMBER: 60/163,682  
; EARLIER FILING DATE: 1999-11-05  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 348  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-457-646-14

Query Match 100.0%; Score 383; DB 4; Length 342;  
Best Local Similarity 100.0%; Pred. No. 3 1e-41;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFGPVDPVDEELTRDLEKHCRCRMEASQKKNWDFQNHKPLEGKYEWQVEVK 60  
DB 22 EHPKPSACNLFGPVDPVDEELTRDLEKHCRCRMEASQKKNWDFQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67  
DB 82 GSLPEFY 88

RESULT 14  
US-09-457-568-6  
; Sequence 6, Application US/09457568  
; Patent No. 6413943  
; GENERAL INFORMATION:  
; APPLICANT: McArthur, James G  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Finer, Mitchell H  
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of  
; TITLE OF INVENTION: Smooth Muscle Cells  
; FILE REFERENCE: 106482.691  
; CURRENT APPLICATION NUMBER: US/09/457,568  
; CURRENT FILING DATE: 1999-12-09  
; EARLIER APPLICATION NUMBER: 60/122,974  
; EARLIER FILING DATE: 1999-03-01  
; EARLIER APPLICATION NUMBER: 60/163,682  
; EARLIER FILING DATE: 1999-11-05  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 365  
; TYPE: PRT

ORGANISM: Homo sapiens  
US-09-457-568-5

Query Match 100.0%; Score 383; DB 4; Length 365;  
Best Local Similarity 100.0%; Pred. No. 3 3e-41;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFGPVDPVDEELTRDLEKHCRCRMEASQKKNWDFQNHKPLEGKYEWQVEVK 60  
DB 32 EHPKPSACNLFGPVDPVDEELTRDLEKHCRCRMEASQKKNWDFQNHKPLEGKYEWQVEVK 91

QY 61 GSLPEFY 67  
DB 92 GSLPEFY 98

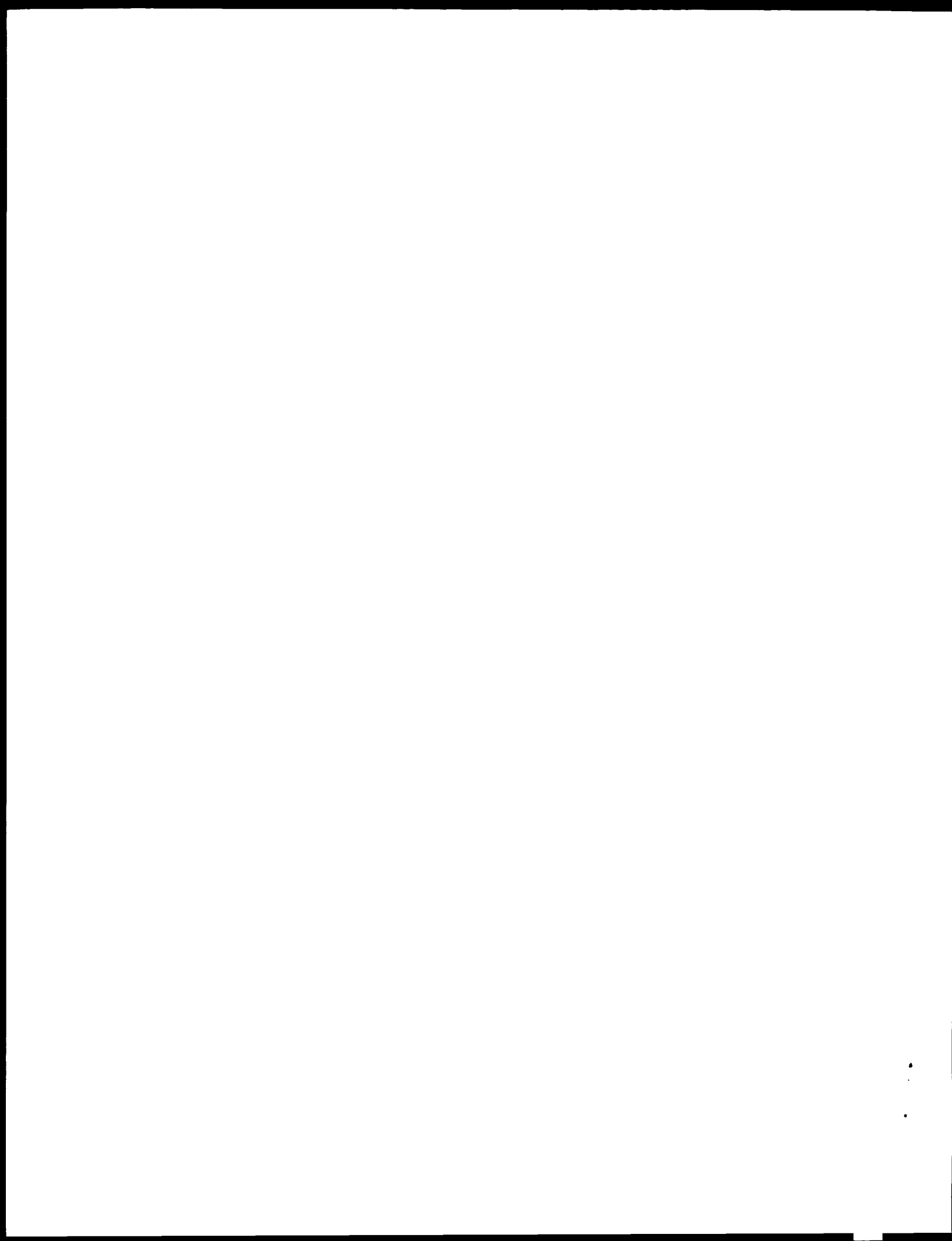
RESULT 15  
US-09-457-568-10  
; Sequence 10, Application US/09457568  
; Patent No. 6413943  
; GENERAL INFORMATION:  
; APPLICANT: McArthur, James G  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Finer, Mitchell H  
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of  
; TITLE OF INVENTION: Smooth Muscle Cells  
; FILE REFERENCE: 106482.691  
; CURRENT APPLICATION NUMBER: US/09/457,568  
; CURRENT FILING DATE: 1999-12-09  
; EARLIER APPLICATION NUMBER: 60/122,974  
; EARLIER FILING DATE: 1999-03-01  
; EARLIER APPLICATION NUMBER: 60/163,682  
; EARLIER FILING DATE: 1999-11-05  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-457-568-10

Query Match 100.0%; Score 383; DB 4; Length 365;  
Best Local Similarity 100.0%; Pred. No. 3 3e-41;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFGPVDPVDEELTRDLEKHCRCRMEASQKKNWDFQNHKPLEGKYEWQVEVK 60  
DB 189 EHPKPSACNLFGPVDPVDEELTRDLEKHCRCRMEASQKKNWDFQNHKPLEGKYEWQVEVK 248

QY 61 GSLPEFY 67  
DB 249 GSLPEFY 255

Search completed May 30, 2003, 09:03:43  
Job time : 6.02067 secs



GenCore version 5.1.6  
Copyright (C) 1993 2003 Compugen Ltd

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:54:42 : Search time = 2962 seconds  
(without alignments)  
1144.739 Million cell updates/sec

Title: US-09-865-018b-2\_copy\_22\_88

Perfect score: 383  
Sequence: 1 EHPKPSACRNLPSPVHEETIPLEKHTIMEFASQKWNFIQNHKPIEKYEWGFVEK 67  
PUEGKYEPWQFVKESTPEFY 67

Scoring table: BLOSUM62  
Gapop 10 0 Gapext 0.5

Searched: 28224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283234

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR73:

1: pir1:

2: pir2:

3: pir3:

4: pir4:

Prod. No. is the number of results predicted by chosen to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	380	99.2	198	2	152718
2	369	96.3	197	2	149064
3	182	47.5	316	2	932424
4	178	46.5	210	2	151683
5	174	45.4	348	2	149262
6	160	41.8	164	2	184725
7	153	39.9	181	2	188674
8	151	39.4	181	2	154380
9	146	38.1	159	2	149023
10	143	37.3	143	2	A49438
11	121.5	31.7	258	2	T34499
12	100	26.1	191	2	T01132
13	88.5	23.1	184	2	T34426
14	70.5	18.4	196	2	T09968
15	69.5	18.1	470	2	S50083
16	69	18.0	196	2	H96532
17	68.5	17.9	209	2	T46140
18	68.5	17.9	611	1	S12566
19	67.6	17.6	246	1	S49770
20	67.5	17.6	489	2	S53431
21	66	17.2	327	2	T30797
22	66	17.2	885	2	138968
23	65.5	17.1	382	1	G01589
24	65	17.0	671	1	OKBOG
25	65	17.0	686	1	S85702
26	65	17.0	903	2	T20804
27	64.5	16.8	570	1	A36954
28	64	16.7	317	2	C73863
29	63.5	16.6	533	2	S52046

30	62	16.2	1094	2	S49313
31	61.5	16.1	279	2	T26166
32	61.5	16.1	388	2	S66728
33	61.5	16.1	633	2	T28788
34	61	15.9	564	2	F87305
35	60.5	15.8	787	2	A72230
36	60.5	15.8	1557	2	T18412
37	60	15.7	153	2	E89850
38	60	15.7	245	2	A62376
39	60	15.7	450	1	A43733
40	60	15.7	1211	2	S65799
41	59.5	15.5	149	2	E69667
42	59.5	15.5	284	2	S37680
43	59.5	15.5	573	2	F94560
44	59.5	15.5	732	2	T40861
45	59	15.4	120	2	AB1425

ALIGNMENTS

RESULT 1

152718

gene p27Kip1 protein - human

C:Species: Homo sapiens (man)

C>Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000

C:Accession: 152718

R:Pieterpol, J.A.; Richlander, S.K.; Sato, Y.; Papadopoulos, N.; Liu, R.; Friedman, C.

Cancer Res. 55, 1206-1210, 1995

A:Title: Assignment of the human p27Kip1 gene to 12p13 and its analysis in leukemias.

A:Reference number: 152718, M01D:95188144; PMID:7882309

A:Accession: 152718

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-198 <RES>

A:Cross-reference: DB S70388, NID:608452, FIIN AA:14-41.1, FID:94261944

C:Genetics:

A:Gene: p27Kip1

A:Introns: 159/1

Query Match 99.2%, Score 380, DB 2, Length 198.

Best Local Similarity 98.5%; Pred. No. 8.9e-36;

Matches 66, Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACRNLPSPVHEETIPLEKHTIMEFASQKWNFIQNHKPIEKYEWGFVEK 60

LL 22 LHPKPSACRNLPSPVHEETIPLEKHTIMEFASQKWNFIQNHKPIEKYEWGFVEK 81

QY 61 GSLEPEFY 67

DB 82 GSLEPEFY 88

RESULT 2

149064

cyclin-cdk inhibitor p27 - mouse

N:A:Alternative names: cdi p27, G1 cyclin cyclin-dependent kinase inhibitor p27

C:Species: Mus musculus (house mouse)

C>Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 05-Nov-1999

C:Accession: 149064

R:Toyoshima, H.; Hunter, T.

Cell 78, 67-74, 1994

A:Title: p27, a novel inhibitor of G1 cyclin-cdk protein kinase activity, is related

A:Reference number: A5489, M01D:9406614; PMID:8334213

A:Accession: 149064

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 1-197 <RES>

A:Cross-reference: FIML:010446, NID:9532771, FIIN AAA21144.1, FID:9532772

C:Keywords: cell cycle control

Query Match 98.3%, Score 369, DB 2, Length 197;

Best Local Similarity 94.0%; Pred. No. 1.6e-34,







[illegible]

Figure 1 illustrates the proposed mechanism for the formation of a 1,2-diol. The process begins with a molecule containing a double bond and a hydroxyl group. This molecule reacts with a reagent (R-OH) to form a cyclic intermediate. This intermediate is then attacked by a nucleophile (Nu<sup>-</sup>) to form a new intermediate. The final step shows the formation of the 1,2-diol product.

Figure 1. The effect of the concentration of the  $\text{H}_2\text{O}_2$  solution on the amount of the  $\text{H}_2\text{O}_2$  consumed in the reaction of the  $\text{H}_2\text{O}_2$  solution with the  $\text{H}_2\text{O}_2$  solution. The concentration of the  $\text{H}_2\text{O}_2$  solution was 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8.0, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9.0, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10.0, 10.1, 10.2, 10.3, 10.4, 10.5, 10.6, 10.7, 10.8, 10.9, 11.0, 11.1, 11.2, 11.3, 11.4, 11.5, 11.6, 11.7, 11.8, 11.9, 12.0, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 12.7, 12.8, 12.9, 13.0, 13.1, 13.2, 13.3, 13.4, 13.5, 13.6, 13.7, 13.8, 13.9, 14.0, 14.1, 14.2, 14.3, 14.4, 14.5, 14.6, 14.7, 14.8, 14.9, 15.0, 15.1, 15.2, 15.3, 15.4, 15.5, 15.6, 15.7, 15.8, 15.9, 16.0, 16.1, 16.2, 16.3, 16.4, 16.5, 16.6, 16.7, 16.8, 16.9, 17.0, 17.1, 17.2, 17.3, 17.4, 17.5, 17.6, 17.7, 17.8, 17.9, 18.0, 18.1, 18.2, 18.3, 18.4, 18.5, 18.6, 18.7, 18.8, 18.9, 19.0, 19.1, 19.2, 19.3, 19.4, 19.5, 19.6, 19.7, 19.8, 19.9, 20.0, 20.1, 20.2, 20.3, 20.4, 20.5, 20.6, 20.7, 20.8, 20.9, 21.0, 21.1, 21.2, 21.3, 21.4, 21.5, 21.6, 21.7, 21.8, 21.9, 22.0, 22.1, 22.2, 22.3, 22.4, 22.5, 22.6, 22.7, 22.8, 22.9, 23.0, 23.1, 23.2, 23.3, 23.4, 23.5, 23.6, 23.7, 23.8, 23.9, 24.0, 24.1, 24.2, 24.3, 24.4, 24.5, 24.6, 24.7, 24.8, 24.9, 25.0, 25.1, 25.2, 25.3, 25.4, 25.5, 25.6, 25.7, 25.8, 25.9, 26.0, 26.1, 26.2, 26.3, 26.4, 26.5, 26.6, 26.7, 26.8, 26.9, 27.0, 27.1, 27.2, 27.3, 27.4, 27.5, 27.6, 27.7, 27.8, 27.9, 28.0, 28.1, 28.2, 28.3, 28.4, 28.5, 28.6, 28.7, 28.8, 28.9, 29.0, 29.1, 29.2, 29.3, 29.4, 29.5, 29.6, 29.7, 29.8, 29.9, 30.0, 30.1, 30.2, 30.3, 30.4, 30.5, 30.6, 30.7, 30.8, 30.9, 31.0, 31.1, 31.2, 31.3, 31.4, 31.5, 31.6, 31.7, 31.8, 31.9, 32.0, 32.1, 32.2, 32.3, 32.4, 32.5, 32.6, 32.7, 32.8, 32.9, 33.0, 33.1, 33.2, 33.3, 33.4, 33.5, 33.6, 33.7, 33.8, 33.9, 34.0, 34.1, 34.2, 34.3, 34.4, 34.5, 34.6, 34.7, 34.8, 34.9, 35.0, 35.1, 35.2, 35.3, 35.4, 35.5, 35.6, 35.7, 35.8, 35.9, 36.0, 36.1, 36.2, 36.3, 36.4, 36.5, 36.6, 36.7, 36.8, 36.9, 37.0, 37.1, 37.2, 37.3, 37.4, 37.5, 37.6, 37.7, 37.8, 37.9, 38.0, 38.1, 38.2, 38.3, 38.4, 38.5, 38.6, 38.7, 38.8, 38.9, 39.0, 39.1, 39.2, 39.3, 39.4, 39.5, 39.6, 39.7, 39.8, 39.9, 40.0, 40.1, 40.2, 40.3, 40.4, 40.5, 40.6, 40.7, 40.8, 40.9, 41.0, 41.1, 41.2, 41.3, 41.4, 41.5, 41.6, 41.7, 41.8, 41.9, 42.0, 42.1, 42.2, 42.3, 42.4, 42.5, 42.6, 42.7, 42.8, 42.9, 43.0, 43.1, 43.2, 43.3, 43.4, 43.5, 43.6, 43.7, 43.8, 43.9, 44.0, 44.1, 44.2, 44.3, 44.4, 44.5, 44.6, 44.7, 44.8, 44.9, 45.0, 45.1, 45.2, 45.3, 45.4, 45.5, 45.6, 45.7, 45.8, 45.9, 46.0, 46.1, 46.2, 46.3, 46.4, 46.5, 46.6, 46.7, 46.8, 46.9, 47.0, 47.1, 47.2, 47.3, 47.4, 47.5, 47.6, 47.7, 47.8, 47.9, 48.0, 48.1, 48.2, 48.3, 48.4, 48.5, 48.6, 48.7, 48.8, 48.9, 49.0, 49.1, 49.2, 49.3, 49.4, 49.5, 49.6, 49.7, 49.8, 49.9, 50.0, 50.1, 50.2, 50.3, 50.4, 50.5, 50.6, 50.7, 50.8, 50.9, 51.0, 51.1, 51.2, 51.3, 51.4, 51.5, 51.6, 51.7, 51.8, 51.9, 52.0, 52.1, 52.2, 52.3, 52.4, 52.5, 52.6, 52.7, 52.8, 52.9, 53.0, 53.1, 53.2, 53.3, 53.4, 53.5, 53.6, 53.7, 53.8, 53.9, 54.0, 54.1, 54.2, 54.3, 54.4, 54.5, 54.6, 54.7, 54.8, 54.9, 55.0, 55.1, 55.2, 55.3, 55.4, 55.5, 55.6, 55.7, 55.8, 55.9, 56.0, 56.1, 56.2, 56.3, 56.4, 56.5, 56.6, 56.7, 56.8, 56.9, 57.0, 57.1, 57.2, 57.3, 57.4, 57.5, 57.6, 57.7, 57.8, 57.9, 58.0, 58.1, 58.2, 58.3, 58.4, 58.5, 58.6, 58.7, 58.8, 58.9, 59.0, 59.1, 59.2, 59.3, 59.4, 59.5, 59.6, 59.7, 59.8, 59.9, 60.0, 60.1, 60.2, 60.3, 60.4, 60.5, 60.6, 60.7, 60.8, 60.9, 61.0, 61.1, 61.2, 61.3, 61.4, 61.5, 61.6, 61.7, 61.8, 61.9, 62.0, 62.1, 62.2, 62.3, 62.4, 62.5, 62.6, 62.7, 62.8, 62.9, 63.0, 63.1, 63.2, 63.3, 63.4, 63.5, 63.6, 63.7, 63.8, 63.9, 64.0, 64.1, 64.2, 64.3, 64.4, 64.5, 64.6, 64.7, 64.8, 64.9, 65.0, 65.1, 65.2, 65.3, 65.4, 65.5, 65.6, 65.7, 65.8, 65.9, 66.0, 66.1, 66.2, 66.3, 66.4, 66.5, 66.6, 66.7, 66.8, 66.9, 67.0, 67.1, 67.2, 67.3, 67.4, 67.5, 67.6, 67.7, 67.8, 67.9,

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Acquisition: 12499

$$A = M(\lambda_1, \dots, \lambda_n) + \sum_{j=1}^n y_j^* e_j e_j^T \in N(A)$$

A: K<sup>+</sup>; Cl<sup>-</sup>; H<sub>2</sub>O; I<sup>-</sup>; Zn<sup>2+</sup>; W<sup>6+</sup>  
A: P<sup>3-</sup>; S<sup>2-</sup>; Fe<sup>2+</sup>; Cu<sup>2+</sup>; Ni<sup>2+</sup>

$\mathcal{A} = \{A_1, A_2, \dots, A_n\}$

2000

Only  $M_{\text{eff}} = 1$ [illegible]

# REVIEWS

100

[illegible][illegible][illegible][illegible]

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The figure consists of 12 line drawings arranged in two columns of six. The first column shows the progression from an egg to a fledgling. The second column shows the nest with the bird inside, and the bird being fed by its parent. The final drawing shows the bird flying away from the nest.

[illegible]

A; Molecules: 1994; DNA  
A; Reviews: 1991; 1994

$$\sum_{i=1}^n \lambda_i \left( \frac{1}{\lambda_i} \right) = \sum_{i=1}^n 1 = n$$

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 Attention: Mr. J. Edgar Hoover

$\alpha$ : Probability of finding a particle at position  $x$ , given by the wave function  $\psi(x)$ .

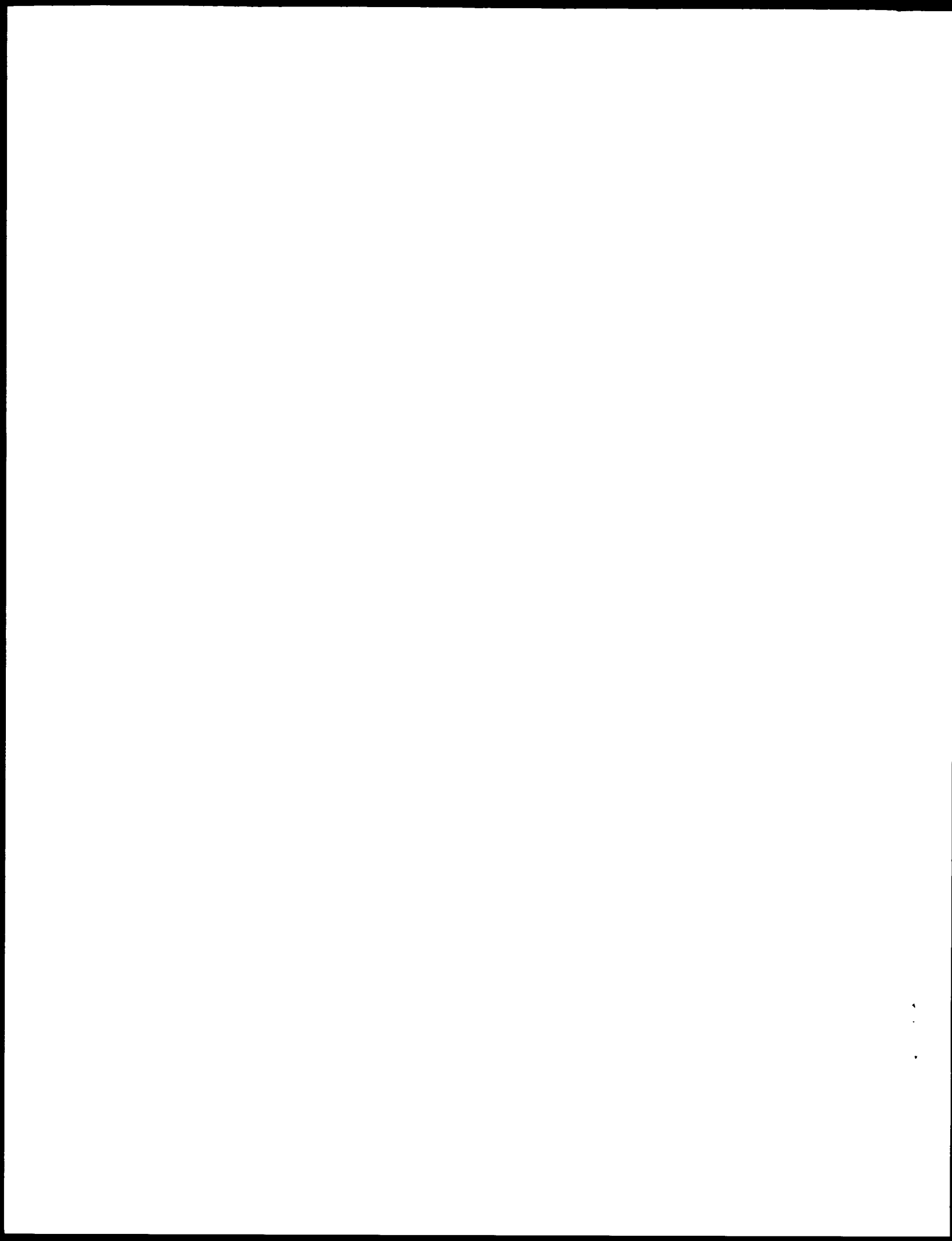
Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group and the experimental group. The control group received a standard diet and water, while the experimental group received a diet supplemented with 0.5% of the active ingredient. The subjects were then subjected to a series of tests: a baseline test, a test with a single dose of the active ingredient, and a test with a repeated dose of the active ingredient. The results of the tests were then compared between the two groups.

[illegible]
$$M_{\text{eff}} = \frac{M}{1 + \frac{1}{\alpha} \left( \frac{1}{\beta} + \frac{1}{\gamma} \right)}$$
A-Miller, J. H. . . . . 242  
A-Miller, J. H. . . . . 242

## References

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 08:52:42 : Search time 28.659 seconds  
(without alignments)  
972.808 Million cell updates/sec

Title: US-09-865-018b-2\_COPY\_22\_88

Perfect score: 383

Sequence: 1 EHPKPSACRNLFPGVDHEEL.....PLEGKYEMQEVKGLPEFY 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	372	97.1	198	1	CDNB_FELCA
3	369	96.3	197	1	CDNB_MOUSE
4	364	95.0	198	1	CDNB_CRICR
5	360	94.0	178	1	CDNB_MOUSE
6	356	93.0	178	1	CDNB_MOUSE
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24	284	75.0	178	1	CDNB_MOUSE
25	280	74.0	178	1	CDNB_MOUSE
26	276	73.0	178	1	CDNB_MOUSE
27	272	72.0	178	1	CDNB_MOUSE
28	268	71.0	178	1	CDNB_MOUSE
29	264	70.0	178	1	CDNB_MOUSE
30	260	69.0	178	1	CDNB_MOUSE
31	256	68.0	178	1	CDNB_MOUSE
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36 58.5 15.3 942 1 15P2\_HUMAN  
37 58 15.1 352 1 VATH\_DROME  
38 58 15.1 761 1 RIR1\_BUCAI  
39 58 15.1 834 1 CASL\_HUMAN  
40 58 15.1 2186 1 YL52\_CAEEL  
41 57.5 15.0 376 1 SPH\_STEPPY  
42 57.5 15.0 490 1 TIME\_ECOLI  
43 57.5 15.0 525 1 NAB2\_YEAST  
44 57.5 15.0 740 1 CATA\_MYCO  
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## ALIGNMENTS

RESULT 1  
CDNB\_HUMAN STANDARD; PRT; 198 AA.  
AC P46527.01-937;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cyclin-dependent kinase inhibitor 1B (cyclin-dependent kinase  
inhibitor p27) (p27Kip1).  
GN CDKN1B OR Kip1  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
PP SEQUENCE FROM N.A., AND SEQUENCE OF 28-79 AND 104-152.  
PC TISSUE=Kidney;  
RX MEDLINE=94306518; PubMed=8033212;  
RA Poljak R, Lee M-H, Erdjument-Bromage H, Koff A, Roberts JM,  
Tempst P., Massague J.;  
RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a  
potential mediator of extracellular antimetabolic signals";  
PL Cell 78:59-66(1994).  
PN [2]  
PP SEQUENCE FROM N.A.  
PC MEDLINE=95184144; PubMed=7882309;  
PA Pietenpol J.A., Bohlender S.K., Sato Y., Papadopoulos N., Liu R.,  
Pietenpol C., Trask P.J., Roberts J.M., Kinzler K.W., Rowley J.D.;  
RT "Assignment of the human p27Kip1 gene to 12p13 and its analysis in  
leukemias";  
PL Cancer Res. 55:1206-1210(1995).  
PN [3]  
PP SEQUENCE FROM N.A., AND VARIANTS TYP-15 AND GLY-109.  
RA Rieder M.J., Braun A.C., Montoya M.A., Chung M.W., Nguyen C.P.,  
Nguyen D.A., Livingston P.J., Poel C.L., Robertson P.D.,  
Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;  
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
PN [4]  
PP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 23-106 OF COMPLEX WITH CDK2  
AND CDCA.  
PC MEDLINE=96300318; PubMed=8684460;  
RA Russo A., Jeffrey P.D., Patten A.K., Massague J., Pavletich N.P.;  
RT "Crystal structure of the p27Kip1 cyclin dependent-kinase inhibitor  
bound to the cyclin A-Cdk2 complex";  
PL Nature 392:385-391(1999).  
CC - FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1  
arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,  
cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin  
NUP50 is required for nuclear import and for degradation of  
phosphorylated p27Kip1 after nuclear import (By similarity).  
CC - SUBUNIT: Interacts with NUP50 (By similarity).  
CC - TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES (PSEUD). HIGHEST  
LEVELS IN SKELETAL MUSCLE, LOWEST IN LIVER AND KIDNEY  
OC - MAIN A PEPTIDE SEQUENCE CONTAINING ONLY AA 28-79 RETAINS  
SUBSTANTIAL KIP1 CYCLIN A/CDK2 INHIBITORY ACTIVITY.

1 SIMILARITY: THE N-TERMINUS OF p27 AND KIP ARE SIMILAR.  
2 NAME: NAME Atlas and/or cytoskeletal proteins. Mammalian  
3 NAME: NAME Atlas and/or cytoskeletal proteins. Mammalian

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9 entities requires a license agreement (see <http://www.ebi.ac.uk/EMBL/seqdb/doc/>  
10 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

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187 EMBL accession: A00004.1  
188 EMBL accession: A00004.1  
189 EMBL accession: A00004.1  
190 EMBL accession: A00004.1

CC NUP50 is required for nuclear import and for degradation of  
CC phosphorylated p27Kip1 after nuclear import.  
CC -1- SUBUNIT: Interacts with NUP50.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
CC  
CC EMBL: U10440; AAA21149.1; -  
CC EMBL: U09968; AAA20235.1; -  
CC MGI: MGI:104565; Cdkn1b.  
CC InterPro: IPR003175; CIP1  
CC Pfam: PF02234; CDI; 1.  
CC Cell cycle; Nuclear protein.  
CC NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
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CC DOMAIN 153 169  
CC FT MGIAGEN 90 90 P-SG, LOSS OF INTERACTION WITH NUP50.  
CC SEQUENCE 197 AA: 22210 MW: 201940-PF02234-500 CQ654;  
CC  
CC Query Match 96.3%, Score 369, DB 1, Length 197.  
CC Best Local Similarity 94.0%; Pred. No. 1e-33;  
CC Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
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CC QY 1 EHPKPSACNLPFGPVHDELTROLEKHCRCMEASORKWNFDFONHKPLECKYEWQVEVK 60  
CC Db 22 EHPKPSACNLPFGPVHDELTROLEKHCRCMEASORKWNFDFONHKPLECKYEWQVEVK 81  
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CC QY 61 GSLPEFY 67  
CC Db 82 GSLPEFY 88  
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CC RESULT 4  
CC CUNB\_CRIGR  
CC ID CUNB\_CRIGR STANDARD; PRT; 198 AA.  
CC AC Q60439;  
CC DT 01-NOV-1997 (Rel. 35, Created)  
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
CC DE Cyclin-dependent kinase inhibitor 1B (Cyclin dependent kinase  
CC inhibitor p27) (p27Kip1) (p27 KIP1);  
CC CDKN1B OR KIP1.  
CC GS Cricetus griseus (Chinese hamster).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
CC Cricetus.  
CC OX NCBI\_TaxID=10029;  
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CC RN FUNCTION:  
CC [1]  
CC  
CC TISSUE=Lung;  
CC MEDLINE=97471701; PubMed=9310642;  
CC RA Vatekh H.P., Pillarsetti K., Kunapuli S., Simpkins H.;  
CC FT Kinase Inhibitory Protein (p27Kip1).  
CC RL Somat. Cell Mol. Genet. 23:147-151(1997)  
CC -1- FUNCTION: Involved in G1 arrest. May mediate TGF beta induced G1  
CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,  
CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin  
CC NUP50 is required for nuclear import and for degradation of  
CC phosphorylated p27Kip1 after nuclear import (By similarity).  
CC -1- SUBUNIT: Interacts with NUP50 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
CC  
CC EMBL: U49649; AAA92570.1; -  
CC InterPro: IPR003175; CIP1  
CC Pfam: PF02234; CDI; 1.  
CC Cell cycle; Nuclear protein.  
CC NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)  
CC  
CC DOMAIN 153 169  
CC FT MGIAGEN 90 90 P-SG, LOSS OF INTERACTION WITH NUP50.  
CC SEQUENCE 197 AA: 22210 MW: 201940-PF02234-500 CQ654;  
CC  
CC Query Match 96.3%, Score 369, DB 1, Length 197.  
CC Best Local Similarity 94.0%; Pred. No. 1e-33;  
CC Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 EHPKPSACNLPFGPVHDELTROLEKHCRCMEASORKWNFDFONHKPLECKYEWQVEVK 60  
CC Db 22 EHPKPSACNLPFGPVHDELTROLEKHCRCMEASORKWNFDFONHKPLECKYEWQVEVK 81  
CC  
CC QY 61 GSLPEFY 67  
CC Db 82 GSLPEFY 88  
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CC RESULT 5  
CC CUNB\_MUSVI  
CC ID CUNB\_MUSVI STANDARD; PRT; 178 AA.  
CC AC P46529;  
CC DT 01-NOV-1995 (Rel. 32, Created)  
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)  
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
CC DE Cyclin-dependent kinase inhibitor 1B (Cyclin dependent kinase  
CC inhibitor p27) (p27Kip1) (Fragment).  
CC CDKN1B.  
CC GS Mus musculus (American mink).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
CC Mustela.  
CC OX NCBI\_TaxID=9667;  
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CC RN FUNCTION:  
CC [1]  
CC  
CC TISSUE=Lung;  
CC MEDLINE=94365518; PubMed=8033212;  
CC RA Polyak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M.,  
CC Tempest P., Massague J.,  
CC FT "Cloning of p27Kip1, a cyclin dependent kinase inhibitor and a  
CC potential mediator of extracellular antimitogenic signals.",  
CC Cell 78:59-66(1994)  
CC  
CC RN [2]  
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CC FUNCTION:  
CC [1]  
CC MEDLINE=94116862; PubMed=8288131;  
CC RA Polyak K., Kato J.-Y., Solomon M.J., Sherr C.J., Massague J.,  
CC Roberts J.M., Koff A.;  
CC FT "p27Kip1, a cyclin-cdk inhibitor, links transforming growth  
CC factor-beta and contact inhibition to cell cycle arrest.",  
CC Genes Dev 8:922(1994)  
CC -1- FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1  
CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,  
CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin  
CC NUP50 is required for nuclear import and for degradation of  
CC phosphorylated p27Kip1 after nuclear import (By similarity).  
CC -1- SUBUNIT: Interacts with NUP50 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.  
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RX MEDLINE=95247028; PubMed 7729484.  
RA Matsuda S., Edwards M.C., Bai C., Parker S., Zhang P., Baldini A.,  
RA Harper J.W., Elledge S.J.;  
RT "p53/KIP2, a structurally distinct member of the p21CIP1 Cdk inhibitor  
RT family, is a candidate tumor suppressor gene.";  
RL Genes Dev. 9:650-662(1995).  
CC -1- FUNCTION: POTENT TIGHT-RINGING INHIBITOR OF SEVERAL G1 CYCLIN/CDK  
CC COMPLEXES (CYCLIN E-CDK2, CYCLIN D2-CDK4, AND CYCLIN A-CDK2) AND,  
CC TO LESSER EXTENT, OF THE MITOTIC CYCLIN B-CDK2. NEGATIVE REGULATOR  
CC OF CELL PROLIFERATION. MAY PLAY A ROLE IN MAINTENANCE OF THE  
CC NONPROLIFERATIVE STATE THROUGHOUT LIFE.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- TISSUE SPECIFICITY: IT IS EXPRESSED IN THE HEART, BRAIN, LUNG,  
CC SKELETAL MUSCLE, KIDNEY, PANCREAS AND TESTIS. HIGH LEVELS ARE SEEN  
CC IN THE PLACENTA WHILE LOW LEVELS ARE SEEN IN THE LIVER.  
CC -----  
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DR EMBL: U20553; AAC52186.1; -  
DR EMBL: U22395; AAA85956.1; -  
DR MGI: 104564; Cdkn1c;  
DR InterPro: IPR03175; CDI.  
DR Pfam: PF02234; CDI; 1.  
KW Cell cycle; Alternative splicing.  
FT DOMAIN 108 189 PRO-RICH.  
FT DOMAIN 178 284 GLU/ASP-RICH.  
FT DOMAIN 309 312 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT VARSPLIC 1 13 MISSING (IN ISOFORM KIP2R/PK7B)  
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QY 4 KPSACNLPFGVHREELTLEKHKEDMERASQKKNFDFONHKPLR--CKYPMQVPRK 61  
DB 28 KSSACRSLEPGVREHFGFELFMFLAFNAFTGNFWLNFEGVLVPLPAPCPPLAWMEVLSE 87  
QY 62 SLPEFY 67  
DB 88 SVAFY 93  
RESULT 8  
CDN1\_HUMAN STARZARD, PRT, 164 AA.  
AC P38936; Q9HUT4;  
DT 01-FEB-1995 (Ref. 31, Created)  
DT 01-FEB-1995 (Ref. 31, last sequence update)  
DT 15-JUN-2002 (Ref. 41, last annotation update)  
DE Cyclin-dependent kinase inhibitor 1 (p21) (CDK-interacting protein 1)  
DE (Melanoma differentiation associated protein 6) (MDA-6).  
GN CDKN1A OR CDKN1 OR CIP1 OR WAF1 OR MIA6 OR SELL OR P21 OR CAP20  
OS Homo sapiens (Human).  
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,  
OC Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.  
OX NCRI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94861996; PubMed 8242751;  
RA Harper J.W., Adami G.R., Wei N., Keyomarsi K., Elledge S.J.;  
RT "The p21 Cdk interacting protein Cipl is a potent inhibitor of G1  
RT cyclin-dependent kinases.";  
RL Cell 75:805-816(1993).  
RN [2]  
RP SEQUENCE FROM N.A.

RX MEDLINE=94061997; PubMed 8243752;  
RA El-Barry W.S., Tokino T., Velculescu V.E., Levy D.R., Parsons P.,  
RA Trent J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.;  
RT "WAF1, a potential mediator of p53 tumor suppression.";  
RL Cell 75:817-825(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94987955; PubMed 8259214;  
RA Xiong Y., Hannon G.J., Zhang H., Casso D., Kobayashi R., Beach D.;  
RT "p21 is a universal inhibitor of cyclin kinases.";  
RL Nature 366:701-704(1993).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Jiang H., Fisher P.B.;  
RT "Use of a sensitive and efficient subtraction hybridization protocol  
RT for the identification of genes differentially regulated during the  
RT induction of differentiation in human melanoma cells.";  
RL Mol. Cell. Differ. 3:245-249(1993).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Jiang H., Liu T., Herlyn M., Kretzel P.S., Weissman B.E.,  
RA Welch P.P., Fisher P.B.;  
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94170884; PubMed 8125163;  
RA Noda A., Ning Y., Venable S.F., Pereira-Smith O.M., Smith J.R.;  
RT "Cloning of senescent cell-derived inhibitors of DNA synthesis using  
RT an expression screen.";  
RL Exp. Cell Res. 211:90-98(1994).  
RN [7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95344154; PubMed 7655464;  
RA Mousses S., Geremek H., Lee P.D., Malkin D., Bull S.B.,  
RA Andralis I.L.;  
RT "Two variants of the CIP1/WAF1 gene occur together and are associated  
RT with human cancer.";  
RL Hum. Mol. Genet. 4:1089-1092(1995).  
RN [8]  
RP SEQUENCE FROM N.A. AND VARIANT ARG-31.  
RA Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,  
RA Nguyen D.A., Livingston R.J., Pool C.L., Robertson P.D.,  
RA Schackwitz W.S., Sherwood J.K., Wittrik A., Nickerson D.A.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A.  
RA Palmer S.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A. AND VARIANT ARG-31.  
RC TISSUE-Eye, and Lung;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 139-160.  
RX MEDLINE=97015085; PubMed 8861913;  
RA Sulbis J.M., Keinan Z., Hurwitz I., O'Donnell M., Kurijan J.;  
RT "Structure of the C-terminal region of p21(WAF1/CIP1) complexed with  
RT human PCNA.";  
PL Cell 87:397-405(1995).  
CC -1- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES  
CC ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO  
CC DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE  
CC ACTIVITY. PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT  
CC KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN ALL ADULT HUMAN TISSUES,  
CC WITH 5-FOLD LOWER LEVELS OBSERVED IN THE BRAIN.  
CC -1- INHIBITION BY P53, MYEYERIN (ANTI-LEUKEMIC COMPOUND) AND INTERFERON  
CC BETA.  
CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.  
CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;  
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/CDKN1AID139.html".





TERMINAL CAP OF mRNA IN PRESENCE OF EIF 4F AND ATP. PROMOTES THE  
ATPASE ACTIVITY AND THE ATP-DEPENDENT RNA-BINDING ACTIVITY OF  
60S RIB A AND EIF4 F.  
1. SUBUNIT: SELF-ASSOCIATES AND INTERACTS WITH EIF4 F70 SUBUNIT.  
2. SIMILARITY: CONTAINS 1 RNA-BINDING DOMAIN (RBD).

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OR SEND AN EMAIL TO LICENSE@SIB.CH).

EMBL: X55743; CAA39265.1;  
FIR: S12566; S12566;  
GENE: HGN: 4285; EIF4F;  
MIR: G04928;  
Info: P100076; rrm; 1;  
SMART: SM00460; RRM; 1;  
PROSITE: PS00102; RRM; 1;  
PROSITE: PS00040; RRM\_RNP; 1;  
KW Protein biosynthesis; Initiation factor; RNA binding.  
FT DOMAIN 96 174 RNA BINDING (RRM).  
FT DOMAIN 164 174  
SV SEQUENCE 411 AA; G0424 MW; 1240009; CR664.

Query Match 17.9% Score 68.5; DB 1; Length 611;  
Best Local Similarity 40.2%; Prot. No. 4.3;  
Matches 16; Conservation 10; Mismatches 24; Indels 5; Gaps 1;

10 RBD: P100076; RBD; 1; Length 611;  
11 RBD: P100076; RBD; 1; Length 611;  
12 RBD: P100076; RBD; 1; Length 611;

## RESULT 13

YMOE YEAST  
A: P54755;  
10 01 OCT 1996 (Ref. 34, Created)  
11 01 OCT 1996 (Ref. 34, Last sequence update)  
12 01 NOV 1997 (Ref. 35, Last annotation update)  
13 01 NOV 1997 (Ref. 35, Last annotation update)  
14 01 NOV 1997 (Ref. 35, Last annotation update)  
15 01 NOV 1997 (Ref. 35, Last annotation update)  
16 01 NOV 1997 (Ref. 35, Last annotation update)  
17 01 NOV 1997 (Ref. 35, Last annotation update)  
18 01 NOV 1997 (Ref. 35, Last annotation update)  
19 01 NOV 1997 (Ref. 35, Last annotation update)  
20 01 NOV 1997 (Ref. 35, Last annotation update)  
21 01 NOV 1997 (Ref. 35, Last annotation update)  
22 01 NOV 1997 (Ref. 35, Last annotation update)  
23 01 NOV 1997 (Ref. 35, Last annotation update)  
24 01 NOV 1997 (Ref. 35, Last annotation update)  
25 01 NOV 1997 (Ref. 35, Last annotation update)  
26 01 NOV 1997 (Ref. 35, Last annotation update)  
27 01 NOV 1997 (Ref. 35, Last annotation update)  
28 01 NOV 1997 (Ref. 35, Last annotation update)  
29 01 NOV 1997 (Ref. 35, Last annotation update)  
30 01 NOV 1997 (Ref. 35, Last annotation update)

EMBL: X55743; CAA39265.1;  
FIR: S12566; S12566;  
GENE: HGN: 4285; EIF4F;  
MIR: G04928;  
Info: P100076; rrm; 1;  
SMART: SM00460; RRM; 1;  
PROSITE: PS00102; RRM; 1;  
PROSITE: PS00040; RRM\_RNP; 1;  
KW Protein biosynthesis; Initiation factor; RNA binding.  
FT DOMAIN 96 174 RNA BINDING (RRM).  
FT DOMAIN 164 174  
SV SEQUENCE 411 AA; G0424 MW; 1240009; CR664.

Query Match 17.9% Score 68.5; DB 1; Length 611;  
Best Local Similarity 40.2%; Prot. No. 4.3;  
Matches 16; Conservation 10; Mismatches 24; Indels 5; Gaps 1;

10 RBD: P100076; RBD; 1; Length 611;  
11 RBD: P100076; RBD; 1; Length 611;  
12 RBD: P100076; RBD; 1; Length 611;

EMBL: X55743; CAA39265.1;  
FIR: S12566; S12566;  
GENE: HGN: 4285; EIF4F;  
MIR: G04928;  
Info: P100076; rrm; 1;  
SMART: SM00460; RRM; 1;  
PROSITE: PS00102; RRM; 1;  
PROSITE: PS00040; RRM\_RNP; 1;  
KW Protein biosynthesis; Initiation factor; RNA binding.  
FT DOMAIN 96 174 RNA BINDING (RRM).  
FT DOMAIN 164 174  
SV SEQUENCE 411 AA; G0424 MW; 1240009; CR664.

Query Match 17.9% Score 68.5; DB 1; Length 611;  
Best Local Similarity 40.2%; Prot. No. 4.3;  
Matches 16; Conservation 10; Mismatches 24; Indels 5; Gaps 1;

14 P100076; RBD; 1; Length 611;  
15 P100076; RBD; 1; Length 611;  
16 P100076; RBD; 1; Length 611;  
17 P100076; RBD; 1; Length 611;  
18 P100076; RBD; 1; Length 611;  
19 P100076; RBD; 1; Length 611;  
20 P100076; RBD; 1; Length 611;  
21 P100076; RBD; 1; Length 611;  
22 P100076; RBD; 1; Length 611;  
23 P100076; RBD; 1; Length 611;  
24 P100076; RBD; 1; Length 611;  
25 P100076; RBD; 1; Length 611;  
26 P100076; RBD; 1; Length 611;  
27 P100076; RBD; 1; Length 611;  
28 P100076; RBD; 1; Length 611;  
29 P100076; RBD; 1; Length 611;  
30 P100076; RBD; 1; Length 611;

EMBL: X55743; CAA39265.1;  
FIR: S12566; S12566;  
GENE: HGN: 4285; EIF4F;  
MIR: G04928;  
Info: P100076; rrm; 1;  
SMART: SM00460; RRM; 1;  
PROSITE: PS00102; RRM; 1;  
PROSITE: PS00040; RRM\_RNP; 1;  
KW Protein biosynthesis; Initiation factor; RNA binding.  
FT DOMAIN 96 174 RNA BINDING (RRM).  
FT DOMAIN 164 174  
SV SEQUENCE 411 AA; G0424 MW; 1240009; CR664.

Query Match 17.9% Score 68.5; DB 1; Length 611;  
Best Local Similarity 40.2%; Prot. No. 4.3;  
Matches 16; Conservation 10; Mismatches 24; Indels 5; Gaps 1;

10 RBD: P100076; RBD; 1; Length 611;  
11 RBD: P100076; RBD; 1; Length 611;  
12 RBD: P100076; RBD; 1; Length 611;

EMBL: X55743; CAA39265.1;  
FIR: S12566; S12566;  
GENE: HGN: 4285; EIF4F;  
MIR: G04928;  
Info: P100076; rrm; 1;  
SMART: SM00460; RRM; 1;  
PROSITE: PS00102; RRM; 1;  
PROSITE: PS00040; RRM\_RNP; 1;  
KW Protein biosynthesis; Initiation factor; RNA binding.  
FT DOMAIN 96 174 RNA BINDING (RRM).  
FT DOMAIN 164 174  
SV SEQUENCE 411 AA; G0424 MW; 1240009; CR664.

Query Match 17.9% Score 68.5; DB 1; Length 611;  
Best Local Similarity 40.2%; Prot. No. 4.3;  
Matches 16; Conservation 10; Mismatches 24; Indels 5; Gaps 1;

10 RBD: P100076; RBD; 1; Length 611;  
11 RBD: P100076; RBD; 1; Length 611;  
12 RBD: P100076; RBD; 1; Length 611;

EMBL: X55743; CAA39265.1;  
FIR: S12566; S12566;  
GENE: HGN: 4285; EIF4F;  
MIR: G04928;  
Info: P100076; rrm; 1;  
SMART: SM00460; RRM; 1;  
PROSITE: PS00102; RRM; 1;  
PROSITE: PS00040; RRM\_RNP; 1;  
KW Protein biosynthesis; Initiation factor; RNA binding.  
FT DOMAIN 96 174 RNA BINDING (RRM).  
FT DOMAIN 164 174  
SV SEQUENCE 411 AA; G0424 MW; 1240009; CR664.

Query Match 17.9% Score 68.5; DB 1; Length 611;  
Best Local Similarity 40.2%; Prot. No. 4.3;  
Matches 16; Conservation 10; Mismatches 24; Indels 5; Gaps 1;

10 RBD: P100076; RBD; 1; Length 611;  
11 RBD: P100076; RBD; 1; Length 611;  
12 RBD: P100076; RBD; 1; Length 611;

EMBL: X55743; CAA39265.1;  
FIR: S12566; S12566;  
GENE: HGN: 4285; EIF4F;  
MIR: G04928;  
Info: P100076; rrm; 1;  
SMART: SM00460; RRM; 1;  
PROSITE: PS00102; RRM; 1;  
PROSITE: PS00040; RRM\_RNP; 1;  
KW Protein biosynthesis; Initiation factor; RNA binding.  
FT DOMAIN 96 174 RNA BINDING (RRM).  
FT DOMAIN 164 174  
SV SEQUENCE 411 AA; G0424 MW; 1240009; CR664.

Query Match 17.9% Score 68.5; DB 1; Length 611;  
Best Local Similarity 40.2%; Prot. No. 4.3;  
Matches 16; Conservation 10; Mismatches 24; Indels 5; Gaps 1;

10 RBD: P100076; RBD; 1; Length 611;  
11 RBD: P100076; RBD; 1; Length 611;  
12 RBD: P100076; RBD; 1; Length 611;

EMBL: X55743; CAA39265.1;  
FIR: S12566; S12566;  
GENE: HGN: 4285; EIF4F;  
MIR: G04928;  
Info: P100076; rrm; 1;  
SMART: SM00460; RRM; 1;  
PROSITE: PS00102; RRM; 1;  
PROSITE: PS00040; RRM\_RNP; 1;  
KW Protein biosynthesis; Initiation factor; RNA binding.  
FT DOMAIN 96 174 RNA BINDING (RRM).  
FT DOMAIN 164 174  
SV SEQUENCE 411 AA; G0424 MW; 1240009; CR664.

Query Match 17.9% Score 68.5; DB 1; Length 611;  
Best Local Similarity 40.2%; Prot. No. 4.3;  
Matches 16; Conservation 10; Mismatches 24; Indels 5; Gaps 1;

10 RBD: P100076; RBD; 1; Length 611;  
11 RBD: P100076; RBD; 1; Length 611;  
12 RBD: P100076; RBD; 1; Length 611;

DT 21-JUN-1986 (rel. 01, last sequence update)  
DT 15-JUN-2002 (rel. 41, last annotation update)  
DE CGMP-dependent protein kinase I, alpha isozyme (EC 2.7.1.37) (CKK I  
DE alpha) (CGK1-alpha).  
GN PRKGI OR PRKGPIA  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89325623; PubMed=2548620;  
RA Wernet W., Fluckner V., Hofmann F.;  
RT "The cDNA of the two isoforms of bovine cGMP-dependent protein  
RT kinase.";  
RL FEBS Lett. 251:191-196(1989)  
RN [2]  
RX SEQUENCE OF 1117, 89 374 AND 407-676.  
RA MEDLINE=85023073; PubMed=6001741;  
RA Takio K., Wade R.D., Smith S.R., Krebs E.G., Walsh K.A., Titani K.;  
RT "Guanosine cyclic 3',5'-phosphate-dependent protein kinase, a  
RT chimeric protein homologous with two separate protein families.";  
RL Biochemistry 23:4207-4218(1984).  
RN [3]  
RX SEQUENCE OF 13-104.  
RA MEDLINE=83213511; PubMed=6304091;  
RA Takio K., Smith S.R., Walsh K.A., Krebs E.G., Titani K.;  
RT "Amino acid sequence around a 'hinge' region and its  
RT 'autophosphorylation' site in bovine lung cGMP-dependent protein  
RT kinase.";  
RL J. Biol. Chem. 258:5531-5536(1983).  
RN [4]  
RX SEQUENCE OF 373-409.  
RA MEDLINE=82098123; PubMed=6274962;  
RA Hashimoto E., Takio K., Krebs E.G.;  
RT "Amino acid sequence at the ATP-binding site of cGMP-dependent  
RT protein kinase.";  
RL J. Biol. Chem. 257:727-733(1982).  
RN [5]  
RX SEQUENCE OF 78-81, AND CHARACTERIZATION.  
RA MEDLINE=84029406; PubMed=2822399;  
RA Heil W.G., Landgraf W., Hofmann F.;  
RT "A catalytically active fragment of cGMP-dependent protein kinase.  
RT Occupation of its cGMP-binding sites does not affect its  
RT phosphotransferase activity.";  
RL Eur. J. Biochem. 168:117-121(1987)  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated  
CC -!- ENZYME REGULATION: BINDING OF cGMP TO CGK RESULTS IN ENZYME  
CC ACTIVATION.  
CC -!- SUBUNIT: Homodimer, antiparallel and monomer.  
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (SHOWN HERE) AND  
CC CGK1-BETA (AC P21136); ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -!- PTM: 65 kDa monomer is produced by proteolytic cleavage.  
CC -!- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT  
CC IDENTICAL TO THAT OF CAK.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC CGMP SUBFAMILY.  
CC -!- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: X16086; CAA34214.1; -  
DR PIR: A00619; OKBOG.  
DR PIR: S05034; S05034.  
DR HSP: P05132; IATP.  
DR InterPro, IPR000719, Euk\_Pkinase.

DK InterPro; IPR000961; Pkinase\_C.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR002374; CGMP\_kin.  
DR InterPro; IPR000595; cNMP\_binding.  
DR Pfam; PF00027; cNMP\_binding; 2.  
DR Pfam; PF00069; pkinase; 1.  
DR Pfam; PF00433; Pkinase\_C; 1.  
DR PRINTS; PR00104; CGMPKINASE.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR SMART; SM00100; cNMP; 2.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00088; cNMP\_BINDING\_1; 2.  
DR PROSITE; PS00889; cNMP\_BINDING\_2; 2.  
DR PROSITE; PS00042; cNMP\_BINDING\_3; 2.  
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;  
KW cNMP-binding; Acetylation; Phosphorylation; Alternative splicing  
FT INTRAMET 0 0  
FT MOD\_RES 1 1 ACETYLATION.  
FT DISULFID 42 42 INTERCHAIN (WITH DIMER).  
FT MOD\_RES 58 58 PHOSPHORYLATION (AUTO-).  
FT MOD\_RES 72 72 PHOSPHORYLATION (AUTO-).  
FT MOD\_RES 84 84 PHOSPHORYLATION (AUTO-).  
FT DOMAIN 1 101 DIMERIZATION.  
FT NP\_BIND 102 219 CGMP 1.  
FT NP\_BIND 220 340 CGMP 2.  
FT DOMAIN 359 618 PROTEIN KINASE.  
FT NP\_BIND 365 373 ATP (BY SIMILARITY).  
FT BINDING 389 389 ATP (BY SIMILARITY).  
FT ACT\_SITE 483 483 BY SIMILARITY.  
FT SITE 77 78 CLEAVAGE.  
SQ SEQUENCE 670 AA. 76287 MW. A8E37ACFE8A7557D CRC64;

Query Match 17.0%; Score 65; DB 1; Length 670;  
Best Local Similarity 37.8%; Pred. No. 11;  
Matches 17, Conservative 7; Mismatches 13; Indels 8; Gaps 3;

QY 24 LEKHCHOMEAEASOKKWNF-----DFQNHKKPLECKYEMQVEKGS 63  
Db 590 IKRLKRD--NPSERLGNLKNVKTQKHWFEG-FNWEGLRKGL 631

Search completed: May 30, 2003, 08:59:07  
Job time: 4.85659 secs



GenCore version 5.1.6  
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OM proteob. protein search, using sw model

Run on: May 30, 2003, 08:53:57, Search time: 11:486, Seconds  
(without alignments)  
1181:337 Million cell updates/sec

Title: US-09-865-018b-2\_copy\_22\_88  
Perfect score: 383  
Sequence: 1 EHPKPSACENFGFVDEHLL.....FILEVIEWLVEKSLPEFY 67

Scoring table: BLOSUM62

Gapop 10 0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SPTREMBL21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organellae:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriopl:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	383	100.0	158	4	043806
2	383	100.0	198	4	Q9NYG6
3	383	100.0	198	4	Q9B0S6
4	380	99.2	198	4	Q96TF0
5	372	97.1	172	6	Q9RFAF
6	372	97.1	197	11	Q08769
7	372	97.1	197	11	Q35792
8	372	97.1	198	6	Q9BDC3
9	255.5	58.9	179	13	Q90YX4
10	178	46.5	210	13	Q91603
11	175	45.7	209	13	Q91646
12	174	45.4	335	11	Q91V06
13	160	41.8	164	11	Q64315
14	153	39.9	164	4	Q96LE1
15	151	39.4	181	4	Q14010
16	121.5	31.7	258	5	Q22198

0906r5 caenorhabdi  
004154 arabidopsi  
082809 arabidopsi  
Q8W312 drosophila  
Q22197 caenorhabdi  
Q9AV92 nicotiana t  
Q94536 drosophila  
P91654 drosophila  
Q91K55 arabidopsi  
P91668 drosophila  
Q91S28 pisum sativ  
Q91J15 arabidopsi  
Q91R70 arabidopsi  
Q9YF16 nicotiana s  
Q94CM0 arabidopsi  
Q98445 arabidopsi  
Q8XNG5 clostridium  
Q9YU29 human immun  
Q9VC60 drosophila  
Q77670 canis famil  
Q48597 chenopodium  
Q28454 monodelphis  
Q91X90 arabidopsi  
Q94CL9 arabidopsi  
Q9SCR2 arabidopsi  
Q03973 saccharomyc  
Q47326 pseudopenta  
Q9F081 mus musculu  
Q92215 mus musculu

## ALIGNMENTS

RESULT 1

Q43806 PRELIMINARY; PRT; 158 AA.  
AC Q43806;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE P27 kipl protein (fragment).  
GN P27 KIP1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BREAST CARCINOMA;  
EX MEDLINE=96140757; PubMed=8557259;  
FA Ferrando A A, Balbin M, Pendas A M, Velasco G.,  
RA Lopez-Otin C.;  
RT "Mutational analysis of the human cyclin-dependent kinase inhibitor  
P27 kipl in primary breast carcinomas";  
RI Hom Genet. 97:91-94(1996).  
DR EMBL; X84849; CAA59284.1; .  
DR InterPro: IPR003175; CDI.  
DE Pfam: PF02334, CDI, 1.  
FT VARIANT 109, 109 G -> V.  
FT NON\_TER 158 158  
SQ SEQUENCE 158 AA; 17651 MW; L6622905BA2FD150 CRC64;

Query Match 100.0%, Score 383, Length 158;  
Best Local Similarity 100.0%; Pred. No. 1.1e-34;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EHPKPSAT\*ENLFGPVTHHEHJMDLKHCKPMDEASQRKWNFDQNHKPLEGKYEQVEVK 60  
DB 22 EHPKPSAT\*ENLFGPVTHHEHJMDLKHCKPMDEASQRKWNFDQNHKPLEGKYEQVEVK 81  
QY 61 GSILPEFY 67  
|||||||





```

1  EHPKPSACRNLFQGVDPVHEELTRDLKXHCRCRDMEASQKKNWDFONHKPLEGKYEWQVEVK 60
2  I:|||||
3  14  EYPKPSACRNLFQGVDPVHEELTRDLKXHCRCRDMEASQKKNWDFONHKPLEGKYEWQVEVK 73
4  I:|||||
5  61  GSLPEFY 67
6  74  GSLPEFY 80
7
8  RESULT 6
9  Q08769
10 ID Q08769 PRELIMINARY: PPT: 197 AA.
11 AC Q08769
12 DT 01-JUL-1997 (TRENBLrel. 04, Created)
13 DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
14 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
15 DE P27 Kipl.
16 OS Rattus norvegicus (Rat).
17 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
18 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Patus.
19 NCBI_TaxID=10116;
20 RN [1]
21 RP SEQUENCE FROM N.A.
22 RA Kawada M., Yamagoe S., Uehara Y.;
23 Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
24 RN [2]
25 RP SEQUENCE FROM N.A.
26 RA Kawada M., Yamagoe S., Kazuo S., Mizuno S., Uehara Y.;
27 Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
28 RN [3]
29 RP SEQUENCE FROM N.A.
30 RA Kawada M., Yamagoe S., Murakami Y., Suzuki K., Mizuno S., Uehara Y.;
31 Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
32 RN [4]
33 RP SEQUENCE FROM N.A.
34 STRAIN-SPRAGUE-DRAWLEY;
35 RA Dastvan F., Reidy M.A.;
36 Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
37 DR EMBL: D86424; BAA19460.1;
38 DR EMBL: AF015194; AAB71368.1;
39 DR InterPro: IPR003175, CDI: 1;
40 Pfam: PF02234; CDI: 1;
41 SQ SEQUENCE 197 AA; 22139 MW; 557380782248476 CP664;
42
43 Query Match: 97.1%; Score 372; DB 11; Length 197;
44 Best Local Similarity 95.5%; Pred. No. 2.3e-33;
45 Matches 64; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
46
47 QY 1 EHPKPSACRNLFQGVDPVHEELTRDLKXHCRCRDMEASQKKNWDFONHKPLEGKYEWQVEVK 60
48 I:|||||
49 22  EHPKPSACRNLFQGVDPVHEELTRDLKXHCRCRDMEASQKKNWDFONHKPLEGKYEWQVEVK 81
50 I:|||||
51 61  GSLPEFY 67
52 82  GSLPEFY 88
53
54 RESULT 7
55 Q045792
56 ID Q045792 PRELIMINARY: PPT: 197 AA.
57 AC Q045792
58 DT 01-JAN-1998 (TRENBLrel. 05, Created)
59 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
60 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
61 DE P27.
62 OS Rattus norvegicus (Rat).
63 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
64 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Patus.
65 NCBI_TaxID=10116;
66 RN [1]
67 RP SEQUENCE FROM N.A.
68 STRAIN-SPRAGUE-DRAWLEY; TISSUE=SPLEEN;
69 MEDLINE=97361761; PubMed=9218722;
70
71 Query Match: 97.1%; Score 372; DB 6; Length 198;
72 Best Local Similarity 97.0%; Pred. No. 2.3e-33;
73 Matches 65; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
74
75 QY 1 EHPKPSACRNLFQGVDPVHEELTRDLKXHCRCRDMEASQKKNWDFONHKPLEGKYEWQVEVK 60
76 I:|||||
77 22  EHPKPSACRNLFQGVDPVHEELTRDLKXHCRCRDMEASQKKNWDFONHKPLEGKYEWQVEVK 81
78 I:|||||
79 61  GSLPEFY 67
80 82  GSLPEFY 88
81
82 RESULT 9
83 Q090YX4
84 ID Q090YX4 PRELIMINARY: PPT: 179 AA.
85 AC Q090YX4
86 DT 01-DEC-2001 (TRENBLrel. 19, Created)
87 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
88 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
89 DE P27-like cyclin-dependent kinase inhibitor.
90 OS Brachydanio rerio (zebrafish) (zebra danio).
91 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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PA Nomura H., Sawada Y., Fujinaga K., Ohtaki S.;
RT *Cloning and characterization of rat p27Kipl, a cyclin-dependent
RI kinase inhibitor.;;
RI Gene 191:211-218(1997);
DR EMBL: D83792; BAA21561.1;
DR InterPro: IPR003175; CDI: 1;
DR Pfam: PF02234; CDI: 1;
SQ SEQUENCE 197 AA; 22112 MW; 5574837802405584 CP664;
9
Query Match: 97.1%; Score 372; DB 11; Length 197;
Best Local Similarity 95.5%; Pred. No. 2.3e-33;
Matches 64; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
10
QY 1 EHPKPSACRNLFQGVDPVHEELTRDLKXHCRCRDMEASQKKNWDFONHKPLEGKYEWQVEVK 60
11 I:|||||
12 22  EHPKPSACRNLFQGVDPVHEELTRDLKXHCRCRDMEASQKKNWDFONHKPLEGKYEWQVEVK 81
13 I:|||||
14 61  GSLPEFY 67
15 82  GSLPEFY 88
16
17 RESULT 8
18 Q09BDC3
19 ID Q09BDC3 PRELIMINARY: PPT: 198 AA.
20 AC Q09BDC3
21 DT 01-JUN-2001 (TRENBLrel. 17, Created)
22 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
23 DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
24 DE P27Kipl.
25 GN P27Kipl.
26 OS Sus scrofa (Pig).
27 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
28 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
29 NCBI_TaxID=9823;
30 RN [1]
31 RP SEQUENCE FROM N.A.
32 PF01INF-2106146; PubMed-11115398;
33 RA Hirano K., Hirano M., Zeng Y., Nishimura J., Hara K., Muta K.;
34 Nawata H., Kanaike H.;
35 *Cloning and functional expression of a degradation-resistant novel
36 isoform of p27Kipl.;;
37 F1 Biochem J. 353:1-57(2001)
38 DR EMBL: AB031957; BAB39727.1;
39 DR EMBL: AB031355; BAB39725.1;
40 DR EMBL: ARS15766; BAB39726.1;
41 DR InterPro: IPR003175; CDI: 1;
42 Pfam: PF02234; CDI: 1;
43 SQ SEQUENCE 198 AA; 22201 MW; E5B01D225E5BDD5F CP664;
44
45 Query Match: 97.1%; Score 372; DB 6; Length 198;
46 Best Local Similarity 97.0%; Pred. No. 2.3e-33;
47 Matches 65; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
48
49 QY 1 EHPKPSACRNLFQGVDPVHEELTRDLKXHCRCRDMEASQKKNWDFONHKPLEGKYEWQVEVK 60
50 I:|||||
51 22  EHPKPSACRNLFQGVDPVHEELTRDLKXHCRCRDMEASQKKNWDFONHKPLEGKYEWQVEVK 81
52 I:|||||
53 61  GSLPEFY 67
54 82  GSLPEFY 88
55
56 RESULT 9
57 Q090YX4
58 ID Q090YX4 PRELIMINARY: PPT: 179 AA.
59 AC Q090YX4
60 DT 01-DEC-2001 (TRENBLrel. 19, Created)
61 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
62 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
63 DE P27-like cyclin-dependent kinase inhibitor.
64 OS Brachydanio rerio (zebrafish) (zebra danio).
65 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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[4]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; TISSUE=BREAST TUMOR;
RA Strausberg K.;
DR EMBL: AJ276595; CAC16482.1; -
DR EMBL: AF160190; AAF00694.1; -
DR EMBL: BC005412; AAF05412.1; -
DR MGD: MGI:104564; Cdkn1c
DR InterPro: IPR003175; CDI
DR Pfam: PF02234; CDI; 1
KW Kinase.
SQ SEQUENCE 335 AA; 35903 MW; F5C40675287FEB4F CRC64;
    Query Match 45.4%; Score 174; DB 11; Length 335;
    Best Local Similarity 47.0%; Pred. No. 2.9e-11;
    Matches 31; Conservative 12; Mismatches 27; Indels 2; Gaps 1;
QY 4 KPSACPNLFGPVDRHEELTRDLEKHKCKPMEEASQPKWNFDQNHKPLE--GKYEWQVEKGS b1
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
15 RSSACKSLFGPVDRHEELGKELMKLAELNADLNKWDNFQQDVFLKPGKGLWNEVDSE 74
QY 62 SLPEFY 67
Db |||||
75 SVPAFY 80
RESULT 13
ID Q64315 PRELIMINARY; PRT: 164 AA.
AC Q64315;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P21 (WAF1).
GN WAF1 OR CIPL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Belinsky S.A.;
RX MEDLINE=95315858; PubMed=7796420;
RA el-Deiry W.S., Tokino T., Waldman T., Velculescu V., Oliver J.D.,
RA Hurrell M., Hill D.E., Rees J.L., Hamilton S.R., Kinzler K.W.,
RA Vogelstein B.;
RT "Topological control of p21WAF1/CIP1 expression in normal and
RT neoplastic tissues."
RL Cancer Res. 55:2910-2919(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F344/N; TISSUE=LUNG;
RA Belinsky S.A.;
RL Submitted (09-1995) to the EMBL/GenBank/DBJ databases
DR EMBL: U24174; AAC52221.1; -
DR EMBL: I41275; AAC42084.1; -
DR InterPro: IPR003175; CDI
DR Pfam: PF02234; CDI; 1
SQ SEQUENCE 164 AA; 18318 MW; 6057E86045B6435F CRC64;
    Query Match 41.8%; Score 160; DB 11; Length 164;
    Best Local Similarity 42.2%; Pred. No. 4.4e-10;
    Matches 27; Conservative 10; Mismatches 27; Indels 0; Gaps 0.
QY 4 KPSACPNLFGPVDRHEELTRDLEKHKCKPMEEASQPKWNFDQNHKPLEGKYEWQVEKGS b3
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
13 RSSACKSLFGPVDRHEELGKELMKLAELNADLNKWDNFQQDVFLKPGKGLWNEVDSE 72
QY 64 PEFY 67
Db |||
73 PKIY 76
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RESULT 14
Q96LE1
ID Q96LE1 PRELIMINARY; PRT: 164 AA.
AC Q96LE1;
DI 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cyclin-dependent kinase inhibitor isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li L.-C., Zhao H., Dahiya R.;
KI "Cloning and Characterization of p21 Isoform."
RL Submitted (Sep-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY008263; AAG15411.1; -
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1
KW Kinase.
SQ SEQUENCE 164 AA; 17827 MW; 378E002161FB3BD7 CRC64;
    Query Match 39.9%; Score 153; DB 4; Length 164;
    Best Local Similarity 44.3%; Pred. No. 2.6e-09;
    Matches 27; Conservative 10; Mismatches 24; Indels 0; Gaps 0;
QY 7 ACNPLFGPVDRHEELTRDLEKHKCKPMEEASQPKWNFDQNHKPLEGKYEWQVEKGS b6
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 ACNPLFGPVDRHEELTRDLEKHKCKPMEEASQPKWNFDQNHKPLEGKYEWQVEKGS b6
QY 67 Y 67
Db ||
77 Y 77
RESULT 15
Q14310
ID Q14310 PRELIMINARY; PRT: 181 AA.
AC Q14310;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclin-dependent kinase (fragment).
GN CIPL/WAF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TUMOR;
RX MEDLINE=95384154; PubMed=7655464;
RA Moyses S., Givol H., Lee P.D., Malkin D., Bull S.R., Andrusis I.L.;
RT "Two variants of the CIPL/WAF1 gene occur together and are associated
RT with human cancer."
PL Hum. Mol. Genet. 4:1089-1092(1995)
DR EMBL: L47322; AAB59559.1; -
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1
KW Kinase.
RN [2]
RP SEQUENCE FROM N.A.
RA Nonier J.;
SQ SEQUENCE 181 AA; 25083 MW; 4CCFA5112323D4F1 CRC64;
    Query Match 39.4%; Score 151; DB 4; Length 181;
    Best Local Similarity 44.3%; Pred. No. 4.8e-09;
    Matches 27; Conservative 9; Mismatches 25; Indels 0; Gaps 0;
QY 7 ACNPLFGPVDRHEELTRDLEKHKCKPMEEASQPKWNFDQNHKPLEGKYEWQVEKGS b6
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 ACNPLFGPVDRHEELTRDLEKHKCKPMEEASQPKWNFDQNHKPLEGKYEWQVEKGS b6
QY 67 Y 67
```

11 01 Y 01

Generated by mpf001 on: May 30, 2003, 09:01:29  
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XX 06-AUG-1998.  
 PD 03-FEB-1998; 98WO-US01893.  
 PF 03-FEB-1997; 97US-0794002.  
 PR (HUTG-) HITCHINSON CANCER RES CENT FRED.  
 PA Porter PL, Roberts JM.  
 PI WPI: 1998-437612/37.  
 DR N-PSDB; AAV47518.  
 XX Assays for protein p27 inhibiting activation of cyclin E-Cdk2  
 PT complex - useful for, e.g. diagnosis and prognosis of cancer,  
 PT especially breast carcinoma  
 PS Disclosure: Fig 14B; 105pp; English.  
 CC The present sequence represents a 27 kDa protein (p27 or Kip1) which  
 CC inhibits the activation of a cyclin E-cyclin-dependent kinase2 (Cdk2)  
 CC complex. A reduced relative level of kip1 is indicative of a  
 CC hyperproliferative disease (particularly cancer, especially breast  
 CC carcinoma) and also is prognostic for increased risk of death and/or  
 CC recurrence of cancer (and may be used to determine suitable treatments).  
 CC Agents that affect the activity of kip1 can be used to treat  
 CC hyperproliferative conditions, e.g. to stimulate tissue or organ repair  
 CC or to establish cell cultures.  
 CC  
 XX Sequence 197 AA:  
 SO  
 Query Match 100.0%; Score 1051; DB 19; Length 197;  
 Best Local Similarity 100.0%; Pred No. 1 le-101;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSNVVYNSGSPSLERMDARQADHPKPSACRNLEFVNHBELTRDEKHCROMEASORKW 60  
 Db 1 MSNVVYNSGSPSLERMDARQADHPKPSACRNLEFVNHBELTRDEKHCROMEASORKW 60  
 QY 61 NDFQNHKPLEGTEYEWQVEKESLPEFYKPKPKPSACKVLAQESQVSSGRQAVPLIG 120  
 Db 61 NDFQNHKPLEGTEYEWQVEKESLPEFYKPKPKPSACKVLAQESQVSSGRQAVPLIG 120  
 QY 121 SQANSEDRHLVDQMPSSDQAGIAQCPGMRKPPAEPSSQNKFPANPTEENVSQSPN 180  
 Db 121 SQANSEDRHLVDQMPSSDQAGIAQCPGMRKPPAEPSSQNKFPANPTEENVSQSPN 180  
 QY 181 AGIVEQTPKKPKGLRROT 197  
 Db 181 AGIVEQTPKKPKGLRROT 197  
 RESULT 4  
 AAY08819  
 ID AAY08819 standard; Protein: 197 AA.  
 AC AAY08819;  
 XX  
 DT 13-AUG-1999 (first entry)  
 DE Mouse wild type p27 protein.  
 XX  
 KW Activation sequence; transcription factor; murine; p163; p27; treatment;  
 KW binding protein; DNA binding domain; effector gene; disease; infection;  
 KW tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;  
 KW transplant rejection; graft-versus host disease; circulatory disorder;  
 KW blood clot; anaemia; hormonal disorder; CNS injury.  
 XX  
 OS Mus sp  
 XX EP926237-A2.  
 XX PN

PD 30-JUN-1999.  
 XX 12-DEC-1998; 98EP-0123709.  
 XX 20-DEC-1997; 97DE-1056975.  
 PR (HMR1) HOECHST MARION ROUSSEL DEUT GMBH.  
 PA Buerklin A, Eilers M, Sedlacek H.  
 PI WPI: 1999-349238/30.  
 DR  
 XX New nucleic acid construct comprising promoter, transcription factor  
 PT gene, activation sequence and effector gene - useful for gene  
 PT therapy treatment of allergies, inflammation, transplant disorders  
 PT and leukaemia  
 PS Disclosure: Page 49; 90pp; German.  
 CC This invention describes a novel nucleic acid construct comprising the  
 CC following components (a) an activation sequence for the transcription  
 CC of component b, (b) component b which is constructed from component b1  
 CC (a transcription factor activating domain), component b2 (murine p163  
 CC or p27 binding protein) and component b3 (a transcription factor DNA  
 CC binding domain); (c) an activation sequence which is activated by binding  
 CC of the expression product of component (b) and which induces  
 CC transcription of component (d) and (d) an effector gene. The construct,  
 CC preferably in a plasmid or viral vector, or cell can be used to treat a  
 CC disease selected from infections, tumours, leukaemia, autoimmune  
 CC diseases, allergies, arthritis, inflammations, transplant rejection,  
 CC graft-versus-host disease, blood clotting disorders, circulatory  
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence  
 CC represents the murine p27 protein which is used in the method of the  
 CC invention.  
 CC  
 XX Sequence 197 AA:  
 SO  
 Query Match 100.0%; Score 1051; DB 20; Length 197;  
 Best Local Similarity 100.0%; Pred No. 1 le-101;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSNVVYNSGSPSLERMDARQADHPKPSACRNLEFVNHBELTRDEKHCROMEASORKW 60  
 Db 1 MSNVVYNSGSPSLERMDARQADHPKPSACRNLEFVNHBELTRDEKHCROMEASORKW 60  
 QY 61 NDFQNHKPLEGTEYEWQVEKESLPEFYKPKPKPSACKVLAQESQVSSGRQAVPLIG 120  
 Db 61 NDFQNHKPLEGTEYEWQVEKESLPEFYKPKPKPSACKVLAQESQVSSGRQAVPLIG 120  
 QY 121 SQANSEDRHLVDQMPSSDQAGIAQCPGMRKPPAEPSSQNKFPANPTEENVSQSPN 180  
 Db 121 SQANSEDRHLVDQMPSSDQAGIAQCPGMRKPPAEPSSQNKFPANPTEENVSQSPN 180  
 QY 181 AGIVEQTPKKPKGLRROT 197  
 Db 181 AGIVEQTPKKPKGLRROT 197  
 RESULT 5  
 AAY08847  
 ID AAY08847 standard; Protein: 197 AA.  
 AC AAY08847;  
 XX  
 DT 13-AUG-1999 (first entry)  
 DE Murine wild type p27 protein.  
 XX  
 KW p163; murine; p27 inhibitor; p27-induced inhibition; cell proliferation;  
 KW p27 binding domain; Raa binding domain; detection; screening; malignancy;  
 KW tumour; mutant; p27 protein.  
 XX  
 OS Mus sp.





DB 121 SCANSIDRLVDQMPDSSDNCAGLAUCGGMKRPAAEDSSSNRANKTEENVSDGSPN 180  
 QY 181 ACTVEDQPKPKGLRRQT 197  
 DB 181 ACTVEDQPKPKGLRRQT 197  
 RESULT 7  
 ID AAY08811 standard; Protein; 212 AA.  
 AC AAY08811;  
 DT 13-AUG-1999 (first entry)  
 DE Mouse p27 protein consensus sequence.  
 KW Activation sequence; transcription factor; murine; p163; p27; treatment;  
 KW binding protein; DNA binding domain; effector gene; disease; infection;  
 KW tumour leukaemia; autoimmune disease; allergy; arthritis; inflammation;  
 KW transplant rejection; graft-versus-host disease; circulatory disorder;  
 KW blood clot; anaemia; hormonal disorder; CNS injury.  
 OS Mus sp.  
 PN EP926237-A2.  
 PD 30-JUN-1999.  
 PF 12-DEC-1998; 98EP-0123709.  
 PR 20-DEC-1997; 97DE-1056975.  
 PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.  
 PI Buerger A, Eilers M, Sedlacek H;  
 DR WPI; 1999-349238/30.  
 PT New nucleic acid construct comprising promoter, transcription factor  
 PT gene, activation sequence and effector gene - useful for gene  
 PT therapy treatment of allergies, inflammation, transplant disorders  
 PT and leukaemia  
 PS Disclosure; Page 49; 90pp; German.  
 XX  
 CC This invention describes a novel nucleic acid construct comprising the  
 CC following components (a) an activation sequence for the transcription  
 CC of component b, (b) component b which is constructed from component b1  
 CC (a transcription factor activating domain), component b2 (murine p163  
 CC or p27 binding protein) and component b3 (a transcription factor DNA  
 CC binding domain), (c) an activation sequence which is activated by binding  
 CC of the expression product of component (b) and which induces  
 CC transcription of component (d) and (d) an effector gene. The construct,  
 CC preferably in a plasmid or viral vector, or cell can be used to treat a  
 CC disease selected from infections, tumours, leukaemia, autoimmune  
 CC diseases, allergies, arthritis, inflammations, transplant rejection,  
 CC graft-versus-host disease, blood clotting disorders, circulatory  
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence  
 CC represents the murine p27 protein consensus sequence which is used to  
 CC describe the method of the invention.  
 XX  
 SQ Sequence 212 AA:  
 Query Match 96 7%: Score 1016; Pos 20; Length 212;  
 Best Local Similarity 99 0%: Pred No. 5,4e-98;  
 Matches 191, Conservative 0; Mismatches 2; Indels 0; Gaps 0.  
 QY 5 RVSNSSPSLFPMDARQADHPKPSA<sup>1</sup>PNLF<sup>2</sup>FPVNHFE<sup>3</sup>LTPE<sup>4</sup>LK<sup>5</sup>HP<sup>6</sup>MEEA<sup>7</sup>SG<sup>8</sup>KKW<sup>9</sup>NP<sup>10</sup>PF<sup>11</sup> 64  
 DB 1 RVSNSSPSLFPMDARQADHPKPSA<sup>1</sup>KNLF<sup>2</sup>GVNHGEL<sup>3</sup>LKLEK<sup>4</sup>HK<sup>5</sup>MEEA<sup>6</sup>SG<sup>7</sup>KKW<sup>8</sup>NP<sup>9</sup>DF<sup>10</sup> 60

QY 65 QNHKPLRGGK<sup>1</sup>YH<sup>2</sup>QV<sup>3</sup>EP<sup>4</sup>KG<sup>5</sup>SL<sup>6</sup>PE<sup>7</sup>Y<sup>8</sup>RP<sup>9</sup>PK<sup>10</sup>PS<sup>11</sup>ACK<sup>12</sup>YLA<sup>13</sup>ES<sup>14</sup>QV<sup>15</sup>SG<sup>16</sup>KA<sup>17</sup>VL<sup>18</sup>IS<sup>19</sup>QAN<sup>20</sup> 124  
 DB 61 QNHKPLRGGK<sup>1</sup>YH<sup>2</sup>QV<sup>3</sup>EP<sup>4</sup>KG<sup>5</sup>SL<sup>6</sup>PE<sup>7</sup>Y<sup>8</sup>RP<sup>9</sup>PK<sup>10</sup>PS<sup>11</sup>ACK<sup>12</sup>YLA<sup>13</sup>ES<sup>14</sup>QV<sup>15</sup>SG<sup>16</sup>KA<sup>17</sup>VL<sup>18</sup>IS<sup>19</sup>QAN<sup>20</sup> 120  
 QY 125 SEDRLVDQMPDSSDNCAGLAUCGGMKRPAAEDSSSNRANKTEENVSDGSPN 184  
 DB 121 SEDRLVDQMPDSSDNCAGLAUCGGMKRPAAEDSSSNRANKTEENVSDGSPN 180  
 QY 185 EQTPKPKGLRRQT 197  
 DB 181 EQTPKPKGLRRQT 193  
 RESULT 8  
 ID AAY08839 standard; Protein; 212 AA.  
 AC AAY08839;  
 DT 13-AUG-1999 (first entry)  
 DE Murine p27 protein consensus sequence.  
 KW p163; murine; p27 inhibitor; p27-induced inhibition; cell proliferation;  
 KW p27 binding domain; Ran binding domain; detection; screening; malignancy;  
 KW tumour; p27 protein.  
 OS Mus sp.  
 PN EP926236-A1.  
 PD 30-JUN-1999.  
 PF 12-DEC-1998; 98EP-0123708.  
 PR 20-DEC-1997; 97DE-1056975.  
 PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.  
 PI Buerger A, Eilers M, Sedlacek H;  
 DR WPI; 1999-349237/30.  
 PT New p27-inhibiting protein p163 and DNA - useful for detection  
 PT and/or quantification of p163 mRNA  
 PS Disclosure; Page 28; 68pp; German.  
 XX  
 CC This invention describes (1) a protein that inhibits p27 and thereby  
 CC arrests p27-induced inhibition of cell proliferation, (2) the protein of  
 CC (1) comprising at least part of the amino acid sequence of murine p163,  
 CC (3) a protein that can be derived from the protein of (2) by deletion of  
 CC the p27 binding domain or the Ran binding domain, (4) a protein that can  
 CC be derived from the protein of (2) by deletion of all amino acid  
 CC sequences other than the p27 binding domain, (5) a protein that is the  
 CC human or other mammalian species homologue of a protein as in (1)-(4),  
 CC (6) DNA encoding the p163 protein, (7) antibodies and antibody fragments  
 CC that bind to the p27 binding domain of a protein as above, (8) antibodies  
 CC and antibody fragments that bind to the Ran binding domain of a protein  
 CC as above, (9) antisense nucleic acids complementary to portions of the  
 CC DNA of (6) between codons 121 and 467, (10) a nucleic acid construct  
 CC coding for an antisense nucleic acid as in (9) for inhibiting the  
 CC proliferation of a cell, in which DNA coding for the antisense nucleic  
 CC acid sequence is linked to at least one activation sequence and is  
 CC introduced into the target cell as naked DNA or as an insert in a  
 CC vector or viral vector and (11) a nucleic acid construct containing the  
 CC DNA of (6) linked to an activation sequence that permits expression of a  
 CC protein as above in a cell. The DNA of (6) can be used for detection  
 CC and/or quantification of p163 mRNA in cells and/or tissues, preferably by  
 CC Northern blotting, PCR or fluorescent in situ hybridization. The proteins  
 CC can be used to produce antibodies, which can be used to detect the  
 CC corresponding protein in cells, tissues or body fluids. The antisense  
 CC nucleic acids can be used to inhibit cell proliferation in vitro or in

of p27. The p27 clone can be used to screen for substrates that inhibit the interaction between the protein and their cognate binding partners. We previously used a two hybrid system or using an affinity system in which p27 or its p27 binding domain is immobilized on a solid phase, the solid phase is incubated with a test substrate, and the inhibition of the binding of a labeled binding partner of p27 (especially p27 or p40) is measured. Assays for p27 can be used to assess the multiplicity of mutants. This sequence represents the mouse p27 protein consensus sequence which is used to describe the method of the invention.

XX Sequence 212 AA.

Query Match

Host Local Similarity 96.7% Score 1065 18 201 Length 212

Matches 191 Conserved 0 Mismatches 21 Indels 0 Gaps 0

5 RVSRSSTFEMAVZALIRKSAFRLPFIYVNHLELLQLKATCMEASJFANRPF 64

1 RVSRSSTFEMAVZALIRKSAFRLPFIYVNHLELLQLKATCMEASJFANRPF 64

65 UNHRELEFEMVFEFESFELVYVGGGKPSA KVALPSQVSGPQAVQLPSQAN 124

1 UNHRELEFEMVFEFESFELVYVGGGKPSA KVALPSQVSGPQAVQLPSQAN 124

61 UNHRELEFEMVFEFESFELVYVGGGKPSA KVALPSQVSGPQAVQLPSQAN 124

125 SHRELVNMGVGGKPSA KVALPSQVSGPQAVQLPSQAN 124

125 SHRELVNMGVGGKPSA KVALPSQVSGPQAVQLPSQAN 124

121 SHRELVNMGVGGKPSA KVALPSQVSGPQAVQLPSQAN 124

185 EUTKRKRLRQET 197

185 EUTKRKRLRQET 197

181 EUTKRKRLRQET 197

RESULT 9

AAV08614 standard protein, 199 AA.

AAV08614

13 ABL 1999 (1111 001111)

Mouse p27 murine protein 4

Activation sequence: transcription factor, murine p27, p27, protein, binding protein, RNA binding protein, effector of gene expression, inhibition, transcription, autoimmunity, disease, allergy, arthritis, inflammation, transplant rejection, graft rejection, disease, cancer, leukemia, blood cell, cancer, leukemia, disease, CNS, injury, mutant.

Mouse sp.

EP92647 AL

60 JUN 1999

12 DEC 1998 9800 0123709

20 DEC 1997 9716 1056975

(HMR1) HMR1 MARRON ROUSSEL DEPT GMR1

Roche A. Elliott M. Sedbrook H

WPI: 1999 44928740

New molecule and construct comprising promoter, transcription factor, gene, activation sequence and effector gene, and a for gene therapy treatment of all diseases, inflammation, transplant disorders and leukemias

Roche A. Elliott M. Sedbrook H

WPI: 1999 44928740

New molecule and construct comprising promoter, transcription factor, gene, activation sequence and effector gene, and a for gene therapy treatment of all diseases, inflammation, transplant disorders and leukemias

Roche A. Elliott M. Sedbrook H

WPI: 1999 44928740

New molecule and construct comprising promoter, transcription factor, gene, activation sequence and effector gene, and a for gene therapy treatment of all diseases, inflammation, transplant disorders and leukemias

Roche A. Elliott M. Sedbrook H

WPI: 1999 44928740

New molecule and construct comprising promoter, transcription factor, gene, activation sequence and effector gene, and a for gene therapy treatment of all diseases, inflammation, transplant disorders and leukemias

Roche A. Elliott M. Sedbrook H

following components: (a) an activation sequence for the transcription of component (b); (b) component to which is constructed from component (a) (a transcription factor activation factor); component (b) (a transcription factor binding protein); (c) an activation sequence which is activated by binding of the expression product of component (b) and which induces transcription of component (d); and (d) an effector gene. The construct is preferably in a plasmid or viral vector, or cell can be used to treat a disease selected from infectious, tumours, leukemias, autoimmune diseases, allergies, arthritis, inflammation, transplant rejection, graft versus host disease, blood cell, transplant disorders, neurological disorders, anemia, hormonal disorders and CNS injuries. This sequence represents a mutant murine p27 protein which is used to describe the method of the invention.

XX Sequence 199 AA.

Query Match

Host Local Similarity 97.0% Score 1065 18 201 Length 199

Matches 191 Conserved 0 Mismatches 4 Indels 0 Gaps 0

5 RVSRSSTFEMAVZALIRKSAFRLPFIYVNHLELLQLKATCMEASJFANRPF 64

1 RVSRSSTFEMAVZALIRKSAFRLPFIYVNHLELLQLKATCMEASJFANRPF 64

65 UNHRELEFEMVFEFESFELVYVGGGKPSA KVALPSQVSGPQAVQLPSQAN 124

1 UNHRELEFEMVFEFESFELVYVGGGKPSA KVALPSQVSGPQAVQLPSQAN 124

61 UNHRELEFEMVFEFESFELVYVGGGKPSA KVALPSQVSGPQAVQLPSQAN 124

125 SHRELVNMGVGGKPSA KVALPSQVSGPQAVQLPSQAN 124

125 SHRELVNMGVGGKPSA KVALPSQVSGPQAVQLPSQAN 124

121 SHRELVNMGVGGKPSA KVALPSQVSGPQAVQLPSQAN 124

185 EUTKRKRLRQET 197

185 EUTKRKRLRQET 197

181 EUTKRKRLRQET 197

RESULT 10

AAV08614 standard protein, 199 AA.

AAV08614

13 ABL 1999 (1111 001111)

Mouse p27 murine protein 4

Activation sequence: transcription factor, murine p27, p27, protein, binding protein, RNA binding protein, effector of gene expression, inhibition, transcription, transcription, autoimmunity, disease, allergy, arthritis, inflammation, transplant rejection, graft rejection, disease, cancer, leukemia, blood cell, cancer, leukemia, disease, CNS, injury, mutant.

Mouse sp.

EP92647 AL

60 JUN 1999

12 DEC 1998 9800 0123709

20 DEC 1997 9716 1056975

(HMR1) HMR1 MARRON ROUSSEL DEPT GMR1

Roche A. Elliott M. Sedbrook H

WPI: 1999 44928740

New molecule and construct comprising promoter, transcription factor, gene, activation sequence and effector gene, and a for gene therapy treatment of all diseases, inflammation, transplant disorders and leukemias

Roche A. Elliott M. Sedbrook H

WPI: 1999 44928740

New molecule and construct comprising promoter, transcription factor, gene, activation sequence and effector gene, and a for gene therapy treatment of all diseases, inflammation, transplant disorders and leukemias

Roche A. Elliott M. Sedbrook H

WPI: 1999 44928740

New molecule and construct comprising promoter, transcription factor, gene, activation sequence and effector gene, and a for gene therapy treatment of all diseases, inflammation, transplant disorders and leukemias

Roche A. Elliott M. Sedbrook H

CC This invention describes (1) a protein that inhibits p27 and thereby  
 CC arrests p27-induced inhibition of cell proliferation, (2) the protein of  
 CC (1) comprising at least part of the amino acid sequence of murine p163.  
 CC (3) a protein that can be derived from the protein of (2) by deletion of  
 CC the p27 binding domain or the p27 binding domain, (4) a protein that can  
 CC be derived from the protein of (2) by deletion of all amino acid  
 CC sequences other than the p27 binding domain, (5) a protein that is the  
 CC human or other mammalian species homologue of a protein as in (1)-(4),  
 CC (6) DNA encoding the p163 protein, (7) antibodies and antibody fragments  
 CC that bind to the p27 binding domain of a protein as above, (8) antibodies  
 CC and antibody fragments that bind to the p27 binding domain of a protein  
 CC as above, (9) antisense nucleic acids complementary to portions of the  
 CC DNA of (6) between codons 121 and 467, (10) a nucleic acid construct  
 CC coding for an antisense nucleic acid as in (9) for inhibiting the  
 CC proliferation of a cell, in which DNA coding for the antisense nucleic  
 CC acid sequence is linked to at least one activation sequence and is  
 CC introduced into the target cell as naked DNA or as an insert in a  
 CC nonviral or viral vector and (11) a nucleic acid construct containing the  
 CC DNA of (6) linked to an activation sequence that permits expression of a  
 CC protein as above in a cell. The DNA of (6) can be used for detection of a  
 CC and/or quantification of p163 mRNA in cells and/or tissues, preferably by  
 CC Northern blotting, PCR or fluorescent in-situ hybridisation. The proteins  
 CC can be used to produce antibodies, which can be used to detect the  
 CC corresponding protein in cells, tissues or body fluids. The antisense  
 CC nucleic acids can be used to inhibit cell proliferation in vitro or in  
 CC vivo. The proteins can be used to screen for substances that inhibit the  
 CC interaction between the proteins and their cellular binding partners,  
 CC preferably using a two hybrid system or using an affinity system in which  
 CC p163 or its p27-binding domain is immobilised on a solid phase, the solid  
 CC phase is incubated with a test substance, and the inhibition of the  
 CC binding of a labelled binding partner of p163 (especially p27 or p40) is  
 CC measured. Assays for p163 can be used to assess the malignancy of  
 CC tumours. This sequence represents a mutant mouse p27 protein sequence  
 CC isolated from clone #294 which is used to describe the method of the  
 CC invention.

XX Sequence 199 AA;

Query Match 95.6%, Score 1005, DB 20, Length 199;

Best Local Similarity 97.9%; Pred. No. 7=97; Indels 0; Gaps 0;

Matches 189; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 RVNSGPSLEKMDARQADHPKPSACRNLFQPVNHELTROLEKHCROMEASQKRWDF 64  
 DB 1 RVNSGPSLEKMDARQADHPKPSACRNLFQPVNHELTROLEKHCROMEASQKRWDF 60  
 QY 65 QNHKLEBRYEWOEVEKESLPFFYRPPPPKPSACKVLAQSSQVSSQKAVPLIGSAN 124  
 DB 61 QNHKLEBRYEWOEVEKESLPFFYRPPPPKPSACKVLAQSSQVSSQKAVPLIGSAN 120  
 QY 125 SEDRLVQMPDSSDNGAGLAWQCPGMKKKPAAEIASSQNKPAPIEENVSDGSPNAGTV 184  
 DB 121 SEDRLVQMPDSSDNGAGLAWQCPGMKKKPAAEIASSQNKPAPIEENVSDGSPNAGTV 180  
 QY 185 EOTPKKPGILRQOT 197  
 DB 181 EOTPKKPGILRQOT 193  
 RESULT 11  
 AA08815  
 ID AAY08815 standard; Protein: 199 AA.  
 XX AAY08815;  
 AC AAY08815;  
 XX 13-AUG-1999 (first entry)  
 DT 13-AUG-1999 (first entry)  
 XX Mouse p27 mutant protein 4.  
 DE  
 XX Activation sequence; transcription factor; murine; p163; p27; treatment;  
 KW binding protein; DNA binding domain; effector gene; disease; infection;  
 KW tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;  
 KW transplant rejection; graft-versus-host disease; circulatory disorder.

KW blood clot; anaemia; hormonal disorder; CNS injury; mutant.  
 XX Mus sp.  
 OS  
 XX E992E237-A2  
 PN  
 XX 30-JUN-1999.  
 PD  
 XX 12-DEC-1998; 98EP 0123709.  
 PE  
 XX 20-DEC-1997; 97NE-1056975.  
 PP  
 XX (EMRI) HOECHST MARION ROUSSEL, DEUT GMBH.  
 PA  
 XX Buegin A, Eilers M, Sedlacek H;  
 PI  
 XX WPI; 1999-349238/30.  
 DK  
 XX  
 PT New nucleic acid construct comprising promoter, transcription factor  
 PT gene, activation sequence and effector gene - useful for gene  
 PT therapy, treatment of allergies, inflammation, transplant disorders  
 PT and leukaemia  
 PS  
 XX Disclosure, Page 49, 50pp; German.

CC This invention describes a novel nucleic acid construct comprising the  
 CC following components (a) an activation sequence for the transcription  
 CC of component b, (b) component b which is constructed from component b1  
 CC (a transcription factor activating domain), component b2 (murine p163  
 CC or p27 binding protein) and component b3 (a transcription factor DNA  
 CC binding domain); (c) an activation sequence which is activated by binding  
 CC of the expression product of component (b) and which induces  
 CC transcription of component (d) and (d) an effector gene. The construct,  
 CC preferably in a plasmid or viral vector, can be used to treat a  
 CC disease selected from infections, tumours, leukaemia, autoimmune  
 CC diseases, allergies, arthritis, inflammations, transplant rejection,  
 CC graft-versus-host disease, blood clotting disorders, circulatory  
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence  
 CC represents a mutant murine p27 protein which is used to describe the  
 CC method of the invention

XX Sequence 199 AA;

Query Match 95.5%, Score 1004, DB 20, Length 199;

Best Local Similarity 98.4%; Pred. No. 8=97; Indels 0; Gaps 0;

Matches 189; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 VNSGPSLEKMDARQADHPKPSACRNLFQPVNHELTROLEKHCROMEASQKRWDF 65  
 DB 1 VNSGPSLEKMDARQADHPKPSACRNLFQPVNHELTROLEKHCROMEASQKRWDF 60  
 QY 66 QNHKLEBRYEWOEVEKESLPFFYRPPPPKPSACKVLAQSSQVSSQKAVPLIGSAN 125  
 DB 61 QNHKLEBRYEWOEVEKESLPFFYRPPPPKPSACKVLAQSSQVSSQKAVPLIGSAN 120  
 QY 126 EOTPKKPGILRQOT 197  
 DB 121 EOTPKKPGILRQOT 192  
 QY 186 EOTPKKPGILRQOT 197  
 DB 181 EOTPKKPGILRQOT 192  
 RESULT 12  
 AA08843  
 ID AAY08843 standard; Protein: 199 AA.  
 XX AAY08843;  
 AC AAY08843;  
 XX 13-AUG-1999 (first entry)  
 DT 13-AUG-1999 (first entry)  
 XX Murine mutant p27 protein from clone #660.  
 DE







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# OM protein - protein search, using sw model

Run on: May 30, 2003, 08:55:37 Search time: 14.7621 seconds  
(without alignments)  
392.644 Million cell updates/sec

Title: US-09-865-018B-4

Perfect score: 1051  
Sequence: 1 MSNVRVSNSEFLEPMARQ...SPNATVHQLTKKTHKPT 197

Scoring table: R10SUM62  
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

## Database:

Issued\_Patents\_AA:  
1: /cgn2\_6/ptodata/1/aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/aa/PT05.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/aa/backfill1.pep.\*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1051	100.0	197	1	US-08-275-983B-2
2	1051	100.0	197	4	US-09-240-906-8
3	1051	100.0	197	4	US-09-215-221-57
4	1051	100.0	197	4	US-08-794-002-4
5	1042	99.1	197	4	US-08-854-039B-4
6	1040	99.0	197	4	US-08-415-655-6
7	1016	96.7	212	4	US-09-215-221-49
8	1005	95.5	194	4	US-09-215-221-52
9	1004	95.5	194	4	US-09-215-221-53
10	1003.5	95.5	195	4	US-09-215-221-54
11	994	94.6	194	4	US-09-215-221-55
12	948	90.2	180	4	US-09-215-221-55
13	944	89.8	180	4	US-09-215-221-50
14	931	88.6	198	4	US-08-406-248-4
15	931	88.6	198	4	US-08-897-333A-2
16	931	88.6	198	4	US-09-240-906-6
17	931	88.6	198	4	US-08-794-002-2
18	931	88.6	198	4	US-09-457-568-26
19	931	88.6	198	4	US-09-457-568-26
20	926	88.1	391	1	US-08-589-981-2
21	926	88.1	391	4	US-09-457-568-4
22	926	88.1	391	4	US-09-457-568-4
23	924	87.9	198	1	US-08-275-983B-3
24	921	87.6	365	4	US-09-457-568-10
25	921	87.6	365	4	US-09-457-568-10
26	921	87.6	380	4	US-09-457-568-8
27	921	87.6	380	4	US-09-457-568-8

## ALIGNMENTS

28	919	87.4	198	4	US-08-854-039B-4	Sequence 2, Appli
29	914	87.0	365	4	US-09-457-568-6	Sequence 6, Appli
30	914	87.0	365	4	US-09-457-568-6	Sequence 6, Appli
31	855	81.4	178	4	US-08-794-002-6	Sequence 6, Appli
32	855	81.4	178	4	US-08-854-039B-6	Sequence 6, Appli
33	855	81.4	198	1	US-08-275-983B-1	Sequence 1, Appli
34	855	81.4	198	4	US-08-794-002-2	Sequence 2, Appli
35	789	75.1	334	4	US-09-457-568-16	Sequence 16, Appli
36	787.5	74.9	348	4	US-09-457-568-14	Sequence 14, Appli
37	787.5	74.9	348	4	US-09-457-568-14	Sequence 14, Appli
38	787.5	74.9	348	4	US-09-457-568-14	Sequence 14, Appli
39	784	74.6	177	4	US-09-457-568-12	Sequence 12, Appli
40	784	74.6	177	4	US-09-457-568-12	Sequence 12, Appli
41	714	69.4	197	4	US-09-215-221-55	Sequence 15, Appli
42	392	37.3	237	4	US-09-457-568-20	Sequence 20, Appli
43	392	37.3	237	4	US-09-457-568-20	Sequence 20, Appli
44	390	37.1	80	4	US-09-457-568-18	Sequence 18, Appli
45	390	37.1	80	4	US-09-457-568-18	Sequence 18, Appli

## RESULT 1

US-08-275-983B-2

Sequence 2, Application US/08275983B

Patent No. 568665

GENERAL INFORMATION:

APPLICANT: Massague, Joan

APPLICANT: Roberts, James M.

APPLICANT: Koff, Andrew

APPLICANT: Foltz, Kornelia

TITLE OF INVENTION: Isolated p27 protein, Nucleic Acid Molecules

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

AUSTRALIA: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/275,983B

FILING DATE: 13-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/179,045

FILING DATE: 07-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/PACKET NUMBER: M1-0796P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO. 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 197 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: Internal

US-08-275-983B-2

Query Match: 100.0%; Score 1051; DB 1; Length 197;

Best Local Similarity: 100.0%; Pred. No. 2.5e+102;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





Best Local Similarity 100.0%; Pref. No. 2 5e-102;  
Matches 197; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJRLKHKRQMEFASQPKW 60  
DB 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJRLKHKRQMEFASQPKW 60  
QY 61 NFDFOHKKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120  
DB 61 NFDFOHKKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120  
QY 121 SQANSEDRHLVDQMPPSDNNOAGLAEOCGMKRRPAAEDSSSNKRPANTEENVSDGSPN 180  
DB 121 SQANSEDRHLVDQMPPSDNNOAGLAEOCGMKRRPAAEDSSSNKRPANTEENVSDGSPN 180  
QY 181 ACTIVEOTPKKPGRLROT 197  
DB 181 ACTIVEOTPKKPGRLROT 197

## RESULT 5

US-08-854-039B-4  
Sequence 4, Application US/08854039B  
Patent No. 6355774  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Roberts, James M.  
APPLICANT: Koff, Andrew  
APPLICANT: Polyak, Kornelia  
TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS  
NUMBER OF INVENTIONS: PRODUCTION AND USE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
ZIP: 02109-2170  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,039B  
FILING DATE: 09-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-079.04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ. ID NO.: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 197 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-854-039B-4

Query Match 99.1%; Score 1042; DB 4; Length 197;

Best Local Similarity 99.5%; Pref. No. 2 2e-101;  
Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJRLKHKRQMEFASQPKW 60  
DB 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJRLKHKRQMEFASQPKW 60  
QY 61 NFDFOHKKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120  
DB 61 NFDFOHKKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120  
QY 181 ACTIVEOTPKKPGRLROT 197  
DB 181 ACTIVEOTPKKPGRLROT 197

QY 121 SQANSEDRHLVDQMPPSDNNOAGLAEOCGMKRRPAAEDSSSNKRPANTEENVSDGSPN 180

DB 121 SQANSEDRHLVDQMPPSDNNOAGLAEOCGMKRRPAAEDSSSNKRPANTEENVSDGSPN 180

QY 181 ACTIVEOTPKKPGRLROT 197

DB 181 ACTIVEOTPKKPGRLROT 197

## RESULT 6

US-08-415-655-6  
Sequence 6, Application US/08415655  
Patent No. 6023480  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Lee, Mong-hong  
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
TITLE OF INVENTION: p75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/415,655  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/47418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 378-0400  
TELEFAX: (212) 371-5525  
INFORMATION FOR SEQ. ID NO.: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 197 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-415-655-6

Query Match 99.0%; Score 1040; DB 3; Length 197;

Best Local Similarity 99.0%; Pref. No. 3 6e-101;  
Matches 195; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJRLKHKRQMEFASQPKW 60  
DB 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJRLKHKRQMEFASQPKW 60  
QY 61 NFDFOHKKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120  
DB 61 NFDFOHKKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120  
QY 121 SQANSEDRHLVDQMPPSDNNOAGLAEOCGMKRRPAAEDSSSNKRPANTEENVSDGSPN 180  
DB 121 SQANSEDRHLVDQMPPSDNNOAGLAEOCGMKRRPAAEDSSSNKRPANTEENVSDGSPN 180  
QY 181 ACTIVEOTPKKPGRLROT 197  
DB 181 ACTIVEOTPKKPGRLROT 197



APPLICANT: EILERS, MARTIN  
APPLICANT: ROEPGEN, ANDREA  
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
FILE REFERENCE: 026083/0192  
CURRENT APPLICATION NUMBER: US/09/215,221  
CURRENT FILING DATE: 1998-12-18  
PRIOR FILING DATE: 1997-12-20  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 54  
LENGTH: 195  
TYPE: PRT  
ORGANISM: Murine sp  
FEATURE:  
OTHER INFORMATION: mutated p27  
US-09-215-221-54

Query Match 95.5%: Score 1003.5; DB 4; Length 195;  
Best Local Similarity 97.9%; Pred. No. 2,3e-97;  
Matches 191; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 NVKVSNGSPLEKMDARQADHPKPSACRNLFQPVNHEELTRDLKHCROMEDASQKKNF 62  
DB 1 NVKVSNGSPLEKMDARQADHPKPSACRNLFQPVNHEELTRDLKHCROMEDASQKKNF 54  
QY 63 DQNHKPLEGRTKEMOEVERGSLPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 122  
DB 60 DQNHKPLEGRTKEMOEVERGSLPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 119  
QY 123 ANSEDRHLVDQMUSSDNAGLALGQKQKKKRAEDSSQNKANKTEENVSDDSPNAG 184  
DB 120 ANSEDRHLVDQMUSSDNAGLALGQKQKKKRAEDSSQNKANKTEENVSDDSPNAG 179  
QY 183 TVEQTPKKPKGLRRQT 197  
DB 180 TVEQTPKKPKGLRRQT 194

RESULT 11  
US-09-215-221-51  
Sequence 51, Application US/09215221  
Patent No. 6265562  
GENERAL INFORMATION:  
APPLICANT: EILERS, MARTIN  
APPLICANT: ROEPGEN, ANDREA  
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
FILE REFERENCE: 026083/0192  
CURRENT APPLICATION NUMBER: US/09/215,221  
CURRENT FILING DATE: 1998-12-18  
PRIOR FILING DATE: 1997-12-20  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 51  
LENGTH: 194  
TYPE: PRT  
ORGANISM: Murine sp  
FEATURE:  
OTHER INFORMATION: mutated p27  
US-09-215-221-51

Query Match 94.6%: Score 994; DB 4; Length 194;  
Best Local Similarity 96.9%; Pred. No. 2,3e-96;  
Matches 187; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PVSNGSPLEPMARQADHPKPSACRNLFQPVNHEELTRDLKHCROMEDASQKKNF 64  
DB 1 PVSNGSPLEPMARQADHPKPSACRNLFQPVNHEELTRDLKHCROMEDASQKKNF 60

QY 65 QNHKPLEGRTKEMOEVERGSLPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 124  
DB 61 QNHKPLEGRTKEMOEVERGSLPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 120  
QY 125 SEEDRLVDQMUSSDNAGLALGQKQKKKRAEDSSQNKANKTEENVSDDSPNAG 184  
DB 121 SEEDRLVDQMUSSDNAGLALGQKQKKKRAEDSSQNKANKTEENVSDDSPNAG 180  
QY 185 EOTPKPKGLRRQT 197  
DB 181 EOTPKPKGLRRQT 193

RESULT 12  
US-09-215-221-55  
Sequence 55, Application US/09215221  
Patent No. 6265562  
GENERAL INFORMATION:  
APPLICANT: EILERS, MARTIN  
APPLICANT: ROEPGEN, ANDREA  
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
FILE REFERENCE: 026083/0192  
CURRENT APPLICATION NUMBER: US/09/215,221  
CURRENT FILING DATE: 1998-12-18  
PRIOR FILING DATE: 1997-12-20  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 55  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Murine sp  
FEATURE:  
OTHER INFORMATION: mutated p27  
US-09-215-221-55

Query Match 90.2%: Score 948; DB 4; Length 180;  
Best Local Similarity 98.3%; Pred. No. 1,3e-91;  
Matches 177; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 16 MIAWALHPKPSACRNLFQPVNHEELTRDLKHCROMEDASQKKNF 75  
DB 1 MIAWALHPKPSACRNLFQPVNHEELTRDLKHCROMEDASQKKNF 70  
QY 76 WOEVERGSLPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 135  
DB 61 WOEVERGSLPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 120  
QY 136 TVEQTPKKPKGLRRQT 197  
DB 121 TVEQTPKKPKGLRRQT 190

RESULT 13  
US-09-215-221-50  
Sequence 50, Application US/09215221  
Patent No. 6265562  
GENERAL INFORMATION:  
APPLICANT: EILERS, MARTIN  
APPLICANT: ROEPGEN, ANDREA  
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
FILE REFERENCE: 026083/0192  
CURRENT APPLICATION NUMBER: US/09/215,221  
CURRENT FILING DATE: 1998-12-18  
PRIOR FILING DATE: 1997-12-20  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn Ver. 2.1



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OM protein - protein search, using SW model

Run on: May 30, 2003, 08:58:12 : Search time 20.1872 seconds  
(without alignments)  
991.736 Million cell updates/sec

Title: US-09-865-018B-4

1051

Perfect score: 1 MSNVRVNSGSPLEPMADP ..... SPNAGTVGTPTKPGGLPPPT 197

Sequence: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 383519 seqs, 10123694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published\_Applications\_AA\*

1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PC01\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1042	99.1	197	10	US-09-865-018-4	Sequence 4, Appl
2	931	88.6	198	9	US-09-970-561-2	Sequence 2, Appl
3	926	88.1	191	8	US-08-902-572-2	Sequence 2, Appl
4	921	87.6	195	8	US-08-902-572-8	Sequence 8, Appl
5	921	87.6	180	8	US-08-902-572-6	Sequence 2, Appl
6	919	87.4	194	10	US-09-865-018-2	Sequence 6, Appl
7	855	81.4	178	10	US-09-865-018-6	Sequence 6, Appl
8	789	75.1	334	8	US-08-902-572-22	Sequence 22, Appl
9	787	74.9	348	8	US-08-902-572-24	Sequence 24, Appl
10	784	74.6	167	8	US-08-902-572-18	Sequence 18, Appl
11	392	47.3	237	8	US-08-902-572-27	Sequence 27, Appl
12	390	37.1	252	8	US-08-902-572-28	Sequence 28, Appl
13	383	36.4	70	8	US-08-902-572-20	Sequence 20, Appl
14	164	15.6	247	10	US-09-945-297-770	Sequence 770, App
15	163	15.5	164	9	US-09-221-268-3	Sequence 3, Appl
16	163	15.5	164	9	US-09-221-268-5	Sequence 5, Appl
17	163	15.5	164	10	US-09-845-318-24	Sequence 24, Appl
18	163	15.5	164	10	US-09-940-766-2	Sequence 2, Appl
19	103	9.8	191	10	US-09-733-507-2	Sequence 2, Appl

20	103	9.8	191	10	US-09-733-507-10	Sequence 10, Appl
21	96	9.1	520	9	US-09-046-804A-19	Sequence 19, Appl
22	89.5	8.5	212	10	US-09-733-507-12	Sequence 12, Appl
23	89	8.5	265	10	US-09-064-761-34248	Sequence 34248, A
24	86	8.2	405	10	US-09-049-407-64	Sequence 63, Appl
25	85.5	8.1	472	9	US-09-053-407-2	Sequence 2, Appl
26	85.5	8.1	1429	9	US-09-053-407-1	Sequence 1, Appl
27	82	8.1	137	10	US-09-733-507-14	Sequence 14, Appl
28	85	8.1	461	9	US-09-046-804A-2	Sequence 2, Appl
29	85	8.1	1205	9	US-10-164-890-1	Sequence 1, Appl
30	84.5	8.0	314	10	US-09-764-845-44	Sequence 43, Appl
31	84.5	8.0	671	9	US-09-843-187-86	Sequence 86, Appl
32	84.5	8.0	671	9	US-10-174-590-346	Sequence 346, Appl
33	84.5	8.0	671	9	US-10-176-758-346	Sequence 346, Appl
34	84.5	8.0	671	9	US-10-175-737-346	Sequence 346, Appl
35	84.5	8.0	671	9	US-10-173-706-346	Sequence 346, Appl
36	84.5	8.0	671	9	US-10-175-738-346	Sequence 346, Appl
37	84.5	8.0	671	9	US-10-175-752-346	Sequence 346, Appl
38	84.5	8.0	671	9	US-10-176-482-346	Sequence 346, Appl
39	84.5	8.0	671	9	US-10-176-757-346	Sequence 346, Appl
40	84.5	8.0	671	9	US-10-176-913-346	Sequence 346, Appl
41	84.5	8.0	671	9	US-10-180-552-346	Sequence 346, Appl
42	84.5	8.0	671	9	US-10-180-557-346	Sequence 346, Appl
43	84.5	8.0	671	9	US-10-173-700-346	Sequence 346, Appl
44	84.5	8.0	671	9	US-10-174-572-346	Sequence 346, Appl
45	84.5	8.0	671	9	US-10-174-579-346	Sequence 346, Appl

#### ALIGNMENTS

RESULT 1  
US-09-865-018-4  
Sequence 4, Application US/09865018  
Patent No. US2002110846A1  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
Koff, Andrew  
Koff, James M.  
polyak, Kornelia  
TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS PRODUCTION AND USE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 09/865,018  
FILING DATE: 24 May 2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/865,018  
FILING DATE: 09 May 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Kathleen P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-079, 04  
TELEPHONE: 617-832-1000  
FAX: 617-832-7000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 197 amino acids  
TYPE: amino acid  
TOPOLOGY: linear



CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/902,572  
FILING DATE: 29-JUL-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-069,03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-7000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ. ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-902-572-8

Query Match: 87.6%, Score 921, DB 8, Length 365;  
Best Local Similarity 87.2%, Pred. No. 4, 5e-73;  
Matches 170; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 2 SNVSVNSPSLEPMARQADHPKPSACPNLFGPVNHETLPLEKHCPMFEASQPKWN 61  
DB 169 SNVSVNSGPSLFRMHPAPAEHPPKPSACPNLFGPVNHETLPLEKHCPMFEASQPKWN 228  
QY 62 FDFQNHKPLEGKRYEWEVEKSLPEFYPPPPPPKPSACVLAQESQVSGSPQAVPLTGS 121  
DB 229 FDFQNHKPLEGKRYEWEVEKSLPEFYPPPPPPKPSACVLAQESQVSGSPQAVPLTGA 288  
QY 122 QANSEDRHLVDMQPPSSDQAGLAEQCPGMKKRPPRAEDSSSSONKRPANRTEENVSGSPNA 181  
DB 289 PASEDTLVLDPKTPDSQSCGRLAFQCAIRKRPATPDSSSTQANKRANPTFEENVSGSPNA 348  
QY 182 GTVEQTPKKPKGLRRQ 196  
DB 349 GSVEQTPKKPKGLRRR 363

RESULT 5  
US-08-902-572-6  
Sequence 6, Application US/08902572  
Patent No. US20020068706A1  
GENERAL INFORMATION:  
APPLICANT: Gyuris, Jeno  
APPLICANT: Lamphere, Lou  
APPLICANT: Beach, David H.  
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,572  
FILING DATE: 29-JUL-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-069,03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-7000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 380 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-902-572-6

Query Match: 87.6%, Score 921, DB 8, Length 380;  
Best Local Similarity 87.2%, Pred. No. 4, 7e-73;  
Matches 170; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 2 SNVSVNSPSLEPMARQADHPKPSACPNLFGPVNHETLPLEKHCPMFEASQPKWN 61  
DB 184 SNVSVNSGPSLFRMHPAPAEHPPKPSACPNLFGPVNHETLPLEKHCPMFEASQPKWN 243  
QY 62 FDFQNHKPLEGKRYEWEVEKSLPEFYPPPPPPKPSACVLAQESQVSGSPQAVPLTGS 121  
DB 244 FDFQNHKPLEGKRYEWEVEKSLPEFYPPPPPPKPSACVLAQESQVSGSPQAVPLTGA 303  
QY 122 QANSEDRHLVDMQPPSSDQAGLAEQCPGMKKRPPRAEDSSSSONKRPANRTEENVSGSPNA 181  
DB 344 PASEDTLVLDPKTPDSQSCGRLAFQCAIRKRPATPDSSSTQANKRANPTFEENVSGSPNA 363  
QY 182 GTVEQTPKKPKGLRRQ 196  
DB 364 GSVEQTPKKPKGLRRR 378

RESULT 6  
US-09-865-018-2  
Sequence 2, Application US/09865018  
Patent No. US2002011086A1  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Roberts, Joan M.  
APPLICANT: Kofl, Andrew  
APPLICANT: Poljak, Kornelia  
TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS  
PRODUCTION AND USE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/865,018  
FILING DATE: 24-MAY-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,039  
FILING DATE: 09-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-079,04









QY 25 KRSACRNLFGPVNHHETLHGLKKHVMHFASSQWNPVQNHKPLFGYHFWQVEVPSL 84  
 |||||||  
 Db 2 KRSACRNLFGPVNHHETLHGLKKHVMHFASSQWNPVQNHKPLFGYHFWQVEVPSL 61  
 QY 85 PFEYFPPR 93  
 |||||||  
 Db 62 PFEYFPPR 70

## RESULT 14

US-09-925-297-770  
 ; Sequence 770, Application US/09925297  
 ; Patent No. US20020081659A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA105  
 ; CURRENT APPLICATION NUMBER: US/09/925,297  
 ; PRIORITY FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05949  
 ; PRIORITY FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIORITY FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 928  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 770  
 ; LENGTH: 247  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (131)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-09-925-297-770

Query Match 15.6%; Score 164; DB 10; Length 247;  
 Best Local Similarity 30.9%; Pred. No. 7,3e-07;  
 Matches 42; Conservative 16; Mismatches 54; Indels 24; Gaps 2.

QY 3 NVRVNSGSLPEPMAPQADHPKPSACPLFGPVNHHETLPLEKHCMDMEFASQPKWNF 62  
 :|||  
 Db 84 HVRTGMCPS-----FPMHKAQPRIPGVNSEQLSRDGDMAGCIDEAREXWNF 134  
 QY 63 DFQNHKPLEGRYEMOFEVERGSLPEFY-----RPPPKSACKVLAQESQ 107  
 |||||  
 Db 135 DFVTEPLEGDFAMERKRLPLKILYLPFGPMHKAQPRIPGVNSEQLSRDGDMAGCIDEAREXWNF 194  
 QY 108 DVSGSRQAVPLIGSOA 123  
 :|||  
 Db 195 DLISCTIVPRSGEOA 210

## RESULT 15

US-09-221-268-3  
 ; Sequence 3, Application US/09221268A  
 ; Publication No. US20020183509A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fisher, Paul B. and  
 ; APPLICANT: Jiang, Hongping  
 ; APPLICANT: The Trustees of Columbia University in the City of New York  
 ; TITLE OF INVENTION: METHOD FOR GENERATING A SUBTRACTED CDNA LIBRARY AND  
 ; FILE REFERENCE: 0575/43563-B  
 ; CURRENT APPLICATION NUMBER: US/09/221,268A  
 ; PRIORITY FILING DATE: 1998-12-23  
 ; EARLIER APPLICATION NUMBER: 08/316,537  
 ; EARLIER FILING DATE: 1994-09-30  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 164  
 ; TYPE: PRT

; ORGANISM: MDA-6(2)  
 US-09-221-268-3

Query Match 15.5%; Score 163; DB 9; Length 164;  
 Best Local Similarity 34.1%; Pred. No. 5,3e-07;  
 Matches 42; Conservative 15; Mismatches 48; Indels 18; Gaps 3;

QY 17 UAGQADHPKPS-ACRNLFGPVNHHETLHGLKKHVMHFASSQWNPVQNHKPLFGYHFW 75  
 |||  
 Db 7 LVPO--NPGSKARPLFGPVNSEQLSRDTALMAGCTQFAFPMWDFVTEPLESDPA 64  
 QY 76 WQVEKDSLPPEFY-----FPMHKAQPRIPGVNSEQLSRDGDMAGCIDEAREXWNF 120  
 :|||  
 Db 65 WQVEKDSLPPEFY-----FPMHKAQPRIPGVNSEQLSRDGDMAGCIDEAREXWNF 124  
 QY 121 SOA 123  
 ||  
 Db 125 SOA 127

Search completed: May 30, 2003, 09:05:10  
 Job time : 21.1072 secs

100  
100  
100

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Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:54.42, Search time 16.5419 seconds  
(without alignments)  
1144.739 Million cell updates/sec

Title: US-09-865-018B-4

Perfect score: 1051

Sequence: 1 MSNVVSNVSGSPLEPMARQ.....SPNAGTVEQTPKKRGLRKQT 197

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

PIR\_73:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1051	100.0	197	2	149064
2	928	88.3	198	2	152718
3	220	20.9	210	2	151683
4	211.5	20.1	348	2	149262
5	196.5	18.7	316	2	G02424
6	182	17.3	164	2	184725
7	174.5	16.3	159	2	149023
8	171.5	16.3	143	2	A49438
9	164	15.6	181	2	168674
10	162	15.4	181	2	154380
11	141.5	13.5	258	2	T24499
12	117	11.1	184	2	T24496
13	103	9.8	191	2	T01132
14	96	9.1	1277	2	T32731
15	95.5	9.1	570	2	A97238
16	94.5	9.0	1045	2	T18373
17	94.5	9.0	1211	2	T43230
18	92.5	8.8	290	2	T22161
19	92.5	8.8	296	2	T18401
20	92.5	8.8	1217	2	T42625
21	92	8.8	450	1	A4773
22	91.5	8.7	2588	2	T14342
23	90.5	8.6	768	2	H54024
24	90.5	8.6	777	2	H54024
25	90.5	8.6	777	2	H54024
26	90.5	8.6	779	2	E24024
27	90	8.6	374	2	C88734
28	89.5	8.5	575	2	A63716
29	89.5	8.5	1205	2	T13959

30	89	8.5	783	2	A55817	cyclin-dependent k
31	89	8.5	1307	2	T25563	hypothetical prote
32	88.5	8.4	372	2	S23325	gene M2.2 protein
33	88	8.4	246	1	S49770	hypothetical prote
34	86.5	8.2	525	2	T2194	cd35A - rat
35	86.5	8.2	607	2	A43776	drebrin E2 - chick
36	86.5	8.2	694	2	AP251	trAc7 protein
37	86.5	8.2	701	2	S17196	transcription fact
38	86.5	8.2	919	2	A11275	DNA ligase (ATP)
39	86.5	8.2	1004	2	H88562	Protein G07A9.3
40	86.5	8.2	1044	2	S40704	hypothetical prote
41	86.5	8.2	1173	2	T42719	TBR-coordinating
42	86	8.2	383	1	A48232	domain 48k chain
43	86	8.2	495	2	I39062	domain 52k chain
44	86	8.2	611	1	S12565	translation initia
45	85.5	8.1	536	2	H72535	hypothetical prote

## ALIGNMENTS

### RESULT 1

149064

cyclin-cdk inhibitor p27 - mouse

N:Alternate names: CDI p27; G1 cyclin-cyclin-dependent kinase inhibitor p27

C:Species: Mus musculus (house mouse)

C>Date: 09-Mar-1990 #sequence, revision 09-Mar-1990 #text, change 05-Nov-1999

C:Accession: 149064

R:Toyoshima, H.; Hunter, T.

Cell 78, 67-74, 1994

A:Title: p27, a novel inhibitor of G1 cyclin-cdk protein kinase activity, is related

A:Reference number: A54839; M01D-04306510; PMID:8043213

A:Accession: 149064

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197 <RES>

A:Cross-references: EMBL:U06440, NID-J533771, IDA:AA01145.1, PDB:532772

C:Keywords: cell cycle control

Query Match 100.0%; Score 1051; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 2.9e-80;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSNVVSNVSGSPLEPMARQADHPKPSACPNLCFSPVNHEDLPDLKKRPDMEEASQPMW	60
DB	1	MSNVVSNVSGSPLEPMARQADHPKPSACPNLCFSPVNHEDLPDLKKRPDMEEASQPMW	60
QY	61	NFQVQNHKPLBSPYEMQFVFRGSIPEFYRPPPPPPSAKVLAQPSQVSSGSKQAVPIIS	120
DB	61	NFQVQNHKPLBSPYEMQFVFRGSIPEFYRPPPPPPSAKVLAQPSQVSSGSKQAVPIIS	120
QY	121	SOANSEDRHIVDQMPDSSQAGIAKQCPQMKRPPAHRSSQNKPAKPFEPVSSGSPN	180
DB	121	SOANSEDRHIVDQMPDSSQAGIAKQCPQMKRPPAHRSSQNKPAKPFEPVSSGSPN	180
QY	181	AGTVEQTPKKRGLRKQT 197	
DB	181	AGTVEQTPKKRGLRKQT 197	

### RESULT 2

152718

gene p27Kip1 protein - human

C:Species: Homo sapiens (man)

C>Date: 01-Nov-1997 #sequence, revision 01-Nov-1997 #text, change 01-Jul-2000

C:Accession: 152718

R:Platenberg, J. A.; Faldut, S. K.; Sato, Y.; Papadopoulos, N.; Liu, R.; Friedman, C.

Cancer Res. 55, 1206-1210, 1995

A:Title: Assignment of the human p27Kip1 gene to 12p13 and its analysis in leukemias.

A:Reference number: 152718; M01D:05188144; PMID:7682409

A:Accession: 152718

A>Status: preliminary, translated from cDNA/EMBL/DDDBJ

A:Molecule type: DNA









OY 195 ROT 197  
DB 177 IRS 179

## RESULT 13

T01132  
N:Alternatve names: hypothetical protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse ear cress)  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 1b-Feb-2001  
C:Accession: T01132; F84624  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Kelchum, K.A.; Cresty, M.; Haidjou, E.; Sykes,  
submitted to the EMBL Data Library, June 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.  
A:Reference number: 214198  
A:Accession: T01132  
A:Status: translated from GB/EMBL/JRRLJ  
A:Molecule type: DNA  
A:Residues: 1-191 <R00>

A:Cross-references: EMBL AC003640, NID:93242700, PID:93242706  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shen, T.P.; Brinkley, M.; Lowe, G.C.; Fujita, Y.;  
M.J. Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.F.; Mayhew, J.; Tallon, J.;  
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420, MIM:2068497, FMTL 1067157  
A:Accession: F84624  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-191 <STO>  
A:Cross-references: GB AF002433, NID:93242700, PID:93242700, PID:93242700, PID:93242700  
A:Gene: F26B6; Atg23430  
A:Map position: 2  
A:Map position: 66/3; 81/2; 170/2

Query Match 9.8%; Score 103; DB 2; Length 191;  
Best Local Similarity 51.6%; Pred. No. 0.18;  
Matches 16; Conservative 9; Mismatches 6; Indels 0; Gaps 0.

OY 50 KMEASQKKNMFQNKPLGKRYWQVE 80  
DB 161 KQKEKFKKKYNDFEKEKPLEGPEWKLIF 191

## RESULT 14

T32731  
PAR Interacting protein - rat

C:Species: Rattus norvegicus (Norway rat)  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 2b-Oct-1999  
C:Accession: T32731  
R:Comte, P.A.; Ossipow, V.; Schilder, U.  
submitted to the EMBL Data Library, January 1997  
A:Description: Isolation of PIP, a 160 kDa nuclear protein that interacts with the act  
A:Reference number: 221213  
A:Accession: T32731  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1277 <COM>  
A:Cross-references: EMBL:U83590; NID:92252210; PID:92252211; PID:92252211; PID:92252211

Query Match 9.1%; Score 96; DB 2; Length 1277;  
Best Local Similarity 22.5%; Pred. No. 6.7;  
Matches 39; Conservative 30; Mismatches 60; Indels 44; Gaps 6;

OY 32 LEGPVNHELTQIKKHCIMFPASQKKKNHLPQ--NKKPLGKRYWQVEWQSGSLPEERY 89  
DB 1024 VERIVNHELTQIKKHCIMFPASQKKKNHLPQ--NKKPLGKRYWQVEWQSGSLPEERY 1072  
OY 90 RPPRPSACKVLAQFSQVSSKQAVPLINISANSPIHIVIMFISDUNQALAEQUP 149

LD 1073 -----QAMNLLGVPPKSKKNVPPSSQSLSTKRRK 1108  
OY 150 GM-----KKPPAEDSSQKKNPKNTEENVSSPNAVTPEQPKPKPQ 146  
DB 1109 GELPPTKPKPKLPSFGTSEPKASQ--QDVTFPAMPAATQPKQPSSTPKRR 1160

## RESULT 15

A97238

membrane associated methyl-accepting chemotaxis protein (with HAMP domain) [imported]  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 1a-Sep-2001  
C:Accession: A97238  
R:Noelling, J.; Brereton, G.; Campbell, M.V.; Mariani, R.S.; Zeng, Q.; Gibson, R.; L.  
J. Bailey, M.O.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
A:Reference number: A97009, MIM:2145925, PID:2145925  
A:Accession: A97238  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-570 <KUP>  
A:Cross-references: GB AF004437, PID:93242700, PID:93242700, PID:93242700, PID:93242700  
A:Experimental source: Clostridium acetobutylicum AF00824  
C:Gene: CAC2746

Query Match 9.1%; Score 95.5; DB 2; Length 570;  
Best Local Similarity 23.1%; Pred. No. 2.8;  
Matches 34; Conservative 34; Mismatches 60; Indels 19; Gaps 4;

OY 41 LPEDEHCHQMEBASQKKNMFQNKPLGKRYWQVEWQSGSLPEERYPPPSAK 100  
DB 210 LTKDKRNLLEINNVKPKMTEPSSSLPYR-----PPEPPTQSYPIPMACQNVNRI 264  
OY 101 VLAESQVSSKQAVPLINISANSPIHIVIMFISDUNQALAEQUP 160  
DB 265 TLNSQDLSSASSSELSATVEINIS-----KKEITFETKVIAPQ---TFPTSA--- 310  
OY 151 SQGNKPNFTEENVSSPNAVTPEQPKPKPQ 187  
DB 311 SSELTASVEFVNANIELSNIVENS 347

Search completed: May 30, 2003, 09:02:43  
Job time: 18.5439 secs

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## OM protein - protein search, using sw model

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

Run on May 30, 2003, 08:52:42 Search time: 4.74 seconds  
(without alignments)  
972,808 Million cell updates/sec

Title: US-09-865-018b-4

Sequence: 1 MSNRYVNSGSLERMDARQ.....SPNACTVDTTKKPELRROT 197

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query length	ID	Description
1	1051	100.0	197	1 CDNB_MOUSE	P46114 felis musculus
2	962	91.5	198	1 CDNB_MOUSE	P19001 felis silve
3	958	91.2	198	1 CDNB_MOUSE	P06439 cricetus
4	931	88.6	198	1 CDNB_MOUSE	P46527 homo sapien
5	855	81.4	178	1 CDNB_MOUSE	P46522 musc
6	211.5	20.1	348	1 CDNB_MOUSE	P49919 mus muscu
7	196.5	18.7	316	1 CDNB_MOUSE	P49918 mus muscu
8	174.5	16.6	159	1 CDNB_MOUSE	P39689 mus muscu
9	163	15.5	164	1 CDNB_MOUSE	P19002 felis silve
10	159.5	15.2	164	1 CDNB_MOUSE	P19002 felis silve
11	92.5	8.8	1217	1 AP4_MOUSE	P08573 mus muscu
12	92	8.8	450	1 INVU_MOUSE	P14590 lemur calla
13	92	8.8	480	1 ZAP2_MOUSE	P43193 homo sapien
14	92	8.8	1822	1 ZAP2_MOUSE	P43193 homo sapien
15	89.5	8.4	575	1 SPAN_MOUSE	P37663 bacillus su
16	88.5	8.4	372	1 M22_MOUSE	P37663 bacillus su
17	88.5	8.4	619	1 NBL4_MOUSE	P57457 brachydanio
18	86.5	8.2	525	1 M11_MOUSE	P48665 ratu
19	86.5	8.2	701	1 HRF2_MOUSE	P25980 xenopus lae
20	86.5	8.2	919	1 TNL1_MOUSE	P18684 homo sapien
21	86.5	8.2	1231	1 YK13_MOUSE	P18684 homo sapien
22	86	8.2	405	1 DEM4_MOUSE	P08495 homo sapien
23	86	8.2	416	1 NAPS_MOUSE	P04513 homo sapien
24	86	8.2	611	1 IPAB_MOUSE	P23588 homo sapien
25	85.5	8.1	652	1 TPER_MOUSE	P16302 gallus galli
26	85.5	8.1	5430	1 ACF7_MOUSE	P09003 homo sapien
27	85	8.1	384	1 TNO1_MOUSE	P24718 galax
28	85	8.1	817	1 HONB_MOUSE	P01778 musca domestica
29	85	8.1	1066	1 T145_MOUSE	P46677 saccharomyce
30	85	8.1	1205	1 A153_MOUSE	P15072 homo sapien
31	84.5	8.0	559	1 ENL_MOUSE	P00311 homo sapien
32	84	8.0	572	1 TPA1_MOUSE	P03008 drosophila
33	84	8.0	556	1 HIR3_MOUSE	P09671 homo sapien

34	83.5	7.9	233	1 SERA_ENTHI	P21338 entamoeba h
35	83.5	7.9	597	1 TXP1_YEAST	P34417 saccharomyce
36	83.5	7.9	764	1 UBF1_HUMAN	P17480 homo sapien
37	83	7.9	369	1 MX_STRPY	P19946 streptococ
38	83	7.9	937	1 NU98_RAT	P49793 ratu
39	82.5	7.8	735	1 ADDA_RAT	P03028 ratu
40	82.5	7.8	1129	1 B227_MOUSE	P09228 caenorhabd
41	82	7.8	502	1 ATRP_MOUSE	P13457 cytophaga
42	82	7.8	554	1 NBL4_MOUSE	P52963 mus muscu
43	81.5	7.8	432	1 FSH_MOUSE	P35821 mus muscu
44	81.5	7.8	2038	1 FSH_MOUSE	P13709 drosophila
45	81	7.7	352	1 SH32_MOUSE	P02420 mus muscu

## ALIGNMENTS

ID	CDNB_MOUSE	STANDARD	PRT	197 AA
AC	P46114			
DT	01-NOV-1995 (rel. 32, Created)			
DT	01-NOV-1995 (rel. 32, Last sequence update)			
DT	15-NOV-2002 (rel. 41, Last annotation update)			
DE	Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase inhibitor p27) (p27Kip1).			
DE	CDKN1B.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Medline=94306519; PubMed=6033213;			
RX	Toyoshima H., Hunter T.;			
RA	"p27, a novel inhibitor of G1 cyclin Cdk protein kinase activity, is related to p21."			
RT	Cell 78:67-74(1994).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	Medline=94306518; PubMed=6033212;			
RX	Poljak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M.,			
RA	Tempst P., Massague J.;			
RT	"Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a potential mediator of extracellular antimitogenic signals."			
RL	Cell 78:59-66(1994).			
RN	[3]			
RP	INTERACTION WITH NUP50, AND MITOGENESIS.			
RC	STRAIN-BALB/c;			
RX	Medline=20271857; PubMed=10811608.			
RA	Mueller L., Thivee K., Boeglin A., Dickmanns A., Eilers M.;			
RT	"Cyclin E-mediated elimination of p27 requires its interaction with the nuclear pore-associated protein MNPAP60."			
RL	EMBO J. 19:2168-2180(2000).			
CC	"FUNCTION: Involved in G1 arrest. May mediate G1 arrest-induced G1 arrest. Binds to and inhibits complexes formed by cyclin E CDK2, cyclin A-CDK2, and cyclin D1-CDK4 interaction with nucleoprotein NUP50. Is required for nuclear import and for degradation of phosphorylated p27Kip1 after mitotic arrest."			
CC	1. SUBUNIT: Interacts with NUP50.			
CC	2. SIMILARITY: THE N-TERMINAL OF CDK1 AND KIP ARE SIMILAR.			
CC	3. This SWISS PRO entry is copyright. It is prepared through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed, usage by and for commercial entities requires a license agreement from EMBL, www.ebi.ac.uk/embldb/ or send an email to license@ebi.ac.uk.			
CC	EMBL: U10440; AAA21149.1;			



Query Match 91.2%; Score 958; DB 1; Length 198;  
 Best Local Similarity 91.3%; Pred. No. 1, 1e-68;  
 Matches 178; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSNVRVNSGSPSLERMDARQADHPKPSACRNIFGVNHEHLETRLEKHPREMEASQPKW 60  
 1 MSNVRVNSGSPSLERMDARQADHPKPSACRNIFGVNHEHLETRLEKHPREMEASQPKW 60  
 DB 1 MSNVRVNSGSPSLERMDARQADHPKPSACRNIFGVNHEHLETRLEKHPREMEASQPKW 60

QY 61 NEFQNHKPLDEGRTEQWEGVSGSLPEFYRPPRPKRSACKVIAQFSQVSGSKAVPLIG 120  
 61 NEFQNHKPLDEGRTEQWEGVSGSLPEFYRPPRPKRSACKVIAQFSQVSGSKAVPLIG 120  
 DB 61 NEFQNHKPLDEGRTEQWEGVSGSLPEFYRPPRPKRSACKVIAQFSQVSGSKAVPLIG 120

QY 121 SOANSEDPRLVQMPQSSDNGAGTAFQCGCPMPKPRPAERSSQNKANFTFNVSQSTR 180  
 121 SOANSEDPRLVQMPQSSDNGAGTAFQCGCPMPKPRPAERSSQNKANFTFNVSQSTR 180  
 DB 121 SOANSEDPRLVQMPQSSDNGAGTAFQCGCPMPKPRPAERSSQNKANFTFNVSQSTR 180

QY 181 ACTVEQTPKKRPLPR 195  
 181 ACTVEQTPKKRPLPR 195  
 DB 181 ACTVEQTPKKRPLPR 195

RESULT 4  
 CDBN\_HUMAN STANDARD; PRT; 198 AA.  
 AC P46527; Q16307;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase  
 inhibitor p27) (p27kip1).  
 GN CDKN1B OR KIP1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-79 AND 104-152.  
 RC TISSUE-Kidney;  
 RX MEDLINE=94306518; PubMed=8033212;  
 RA Poljak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M.,  
 Tempst P., Massague J.;  
 RT "Cloning of p27kip1, a cyclin dependent kinase inhibitor and a  
 potential mediator of extracellular antimitogenic signals.";  
 RL Cell 78:59-66(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95188144; PubMed=7882309;  
 RA Pietersen J.A., Bohlander S.K., Sato Y., Papadopoulos N., Liu R.,  
 Friedman G., Trask B.J., Roberts J.M., Kinzler K.W., Rowley J.D.;  
 RT "Assignment of the human p27kip1 gene to 12p13 and its analysis in  
 leukemias.";  
 RL Cancer Res. 55:1206-1210(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANTS TRP-15 AND GLY-109  
 RA Rieder M.T., Traut A.C., Motroy M.A., Chung M.-W., Nguyen C.F.,  
 Nguyen D.A., Livingston P.J., Poel G.L., Robertson P.D.,  
 Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson P.A.;  
 RT Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 23-106 OF COMPLEX WITH CDK2  
 AND CG2A.  
 RX MEDLINE=96300318; PubMed=8664460;  
 RA Russo A.A., Jeffrey P.D., Patten A.K., Massague J., Pavletich N.P.;  
 RT "Crystal structure of the p27kip1 cyclin-dependent kinase inhibitor  
 bound to the cyclin A-CDK2 complex.";  
 RL Nature 382:325-331(1996).  
 CC -1- FUNCTION: Involved in G1 arrest. May mediate TGF-beta-induced G1  
 arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,  
 cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin  
 NUP50 is required for nuclear import and for degradation of  
 phosphorylated p27kip1 after nuclear import (By similarity).  
 CC -1- SUBUNIT: Interacts with NUP50 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED. HIGHEST  
 CC LEVELS IN SKELETAL MUSCLE, LOWEST IN LIVER AND KIDNEY.  
 CC -1- DOMAIN: A PEPTIDE SEQUENCE CONTAINING ONLY AA 28-79 RETAINS  
 CC SUBSTANTIAL KIP1 CYCLIN A/CDK2 INHIBITORY ACTIVITY.  
 CC -1- SIMILARITY: THE N-TERMINAL OF KIP1 AND KIP ARE SIMILAR.  
 CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;  
 CC WWW="http://www.infobiogen.fr/services/otrom/databases/CDKN1B1D16.html".  
 CC  
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 CC or send an email to [licensing@sib.ch](mailto:licensing@sib.ch)).

CC EMBL: 010906; AA02040.1; -;  
 CC EMBL: S76988; AAD1424.1; -;  
 CC EMBL: S76986; AAD1424.1; JOINED.  
 CC EMBL: AF480891; AAL7804.1; -;  
 CC PDB: 1J0U; 29-JUL-97.  
 CC DR SWISS-2DPAGE: P46527; HUMAN.  
 CC DR Genew: HGNC:1785; CDKN1B.  
 CC DR MIM: 600778; -;  
 CC DR InterPro: IPR003175; CDI.  
 CC DR Pfam: PF02234; CDI; 1.  
 CC KM Cell cycle: Nuclear protein; 3D structure; Polymorphism.  
 CC FT DOMAIN 153 169 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 CC FT VARIANT 15 15 R > W (IN DASNP 2006928).  
 CC FT /FTID=VAR\_011871.  
 CC FT VARIANT 109 109 V > G (IN DASNP 2006927).  
 CC FT /FTID=VAR\_011872.  
 CC FT SEQUENCE 22 22 F...G (IN SPP 2)  
 CC SV SEQUENCE 198 AA; 22073 MW; 111B058901C6F3FC CXC64;

Query Match 88.6%; Score 931; DB 1; Length 198;  
 Best Local Similarity 87.8%; Pred. No. 1, 4e-66;  
 Matches 172; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSNVRVNSGSPSLERMDARQADHPKPSACRNIFGVNHEHLETRLEKHPREMEASQPKW 60  
 1 MSNVRVNSGSPSLERMDARQADHPKPSACRNIFGVNHEHLETRLEKHPREMEASQPKW 60  
 DB 1 MSNVRVNSGSPSLERMDARQADHPKPSACRNIFGVNHEHLETRLEKHPREMEASQPKW 60

QY 61 NEFQNHKPLDEGRTEQWEGVSGSLPEFYRPPRPKRSACKVIAQFSQVSGSKAVPLIG 120  
 61 NEFQNHKPLDEGRTEQWEGVSGSLPEFYRPPRPKRSACKVIAQFSQVSGSKAVPLIG 120  
 DB 61 NEFQNHKPLDEGRTEQWEGVSGSLPEFYRPPRPKRSACKVIAQFSQVSGSKAVPLIG 120

QY 121 SOANSEDPRLVQMPQSSDNGAGTAFQCGCPMPKPRPAERSSQNKANFTFNVSQSTR 180  
 121 SOANSEDPRLVQMPQSSDNGAGTAFQCGCPMPKPRPAERSSQNKANFTFNVSQSTR 180  
 DB 121 SOANSEDPRLVQMPQSSDNGAGTAFQCGCPMPKPRPAERSSQNKANFTFNVSQSTR 180

QY 181 ACTVEQTPKKRPLPR 196  
 181 ACTVEQTPKKRPLPR 196  
 DB 181 ACTVEQTPKKRPLPR 196

RESULT 5  
 CDBN\_MOUSE STANDARD; PRT; 178 AA.  
 AC P46529;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cyclin-dependent kinase inhibitor 1B (cyclin dependent kinase  
 inhibitor p27) (p27kip1) (Fragment).  
 GN CDKN1B.  
 OS Mus musculus (house mouse).  
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
 CC NCBI\_TaxID=9607;  
 RN [1]  
 RP SEQUENCE FROM N.A.



DE Cyclin-dependent kinase inhibitor 1C (Cyc1in-dependent kinase  
inhibitor p57) (p57kip2).  
GN CDKN1C OR KIP2  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates, Catarrhini, Hominoidea; Homo.  
NCBI\_TaxID=9606;  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=95247028; PubMed=7729684;  
RA Matsuo S., Edwards M.C., Bai C., Parker S., Zhang P., Baldini A.,  
Halter J.W., Ellledge S.J.,  
RT "p57kip2, a structurally distinct member of the p21cip1 Cdk inhibitor  
family, is a candidate tumor suppressor gene.";  
RT Genes Dev 9:650-662(1995).  
RN (2)  
RP SEQUENCE FROM N.A.  
RA Reid L.H., Crider-Miller S.J., West A., Lee M.H., Massague J.,  
RL Weissman B.E.;  
RN Submitted (MAR-1996) to the EMBL/GenBank/TrnB databases  
RN (3)  
RP SEQUENCE OF 12,316 FROM N.A., AND VARIANTS.  
RX MEDLINE=96209309; PubMed=8655143;  
RA Tokino T., Ueno T., Furuhata T., Matsushima M., Miyatsu T.,  
RA Sasaki S., Nakamura Y.;  
RT "Characterization of the human p57kip2 gene: alternative splicing,  
insertion/deletion polymorphisms in VNR sequences in the coding  
region, and mutational analysis.";  
RT Hum. Genet. 97:625-631(1996).  
CC -1- FUNCTION: POTENT TIGHT-RINGING INHIBITOR OF SEVERAL CDK CYCLIN/CDK  
COMPLEXES: CYCLIN E-CDK2, CYCLIN D2-CDK4 AND CYCLIN A-CDK2 AND,  
TO LESSER EXTENT OF THE MITOTIC CYCLIN B-CDK2 NEGATIVE REGULATOR  
OF CELL PROLIFERATION. MAY PLAY A ROLE IN MAINTENANCE OF THE  
NONPROLIFERATIVE STATE THROUGHOUT LIFE.  
CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).  
CC -1- TISSUE SPECIFICITY: IT IS EXPRESSED IN THE HEART, BRAIN, LUNG,  
SKELETAL MUSCLE, KIDNEY, PANCREAS AND TESTIS. HIGH LEVELS ARE SEEN  
IN THE PLACENTA WHILE LOW LEVELS ARE SEEN IN THE LIVER.  
CC -1- DISEASE: CDKN1C MUTATIONS ARE INVOLVED IN TUMOR FORMATION.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL, mutation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL: 023398; AAB5095.1;  
DR EMBL: 048669; AAB05896.1;  
DR EMBL: D64137; BAAL1014.1;  
DR EMBL: D64137; BAAL1015.1;  
DR Genew: HGNC:1786; CDKN1C.  
DR MIM: 600856;  
DR InterPro, IPR003175; CDT1.  
DR Pfam, PF02234; CDT1.  
KW Cell cycle; Anticarcinogenic; Alternative splicing; Disease mutation;  
FT Repeat. 156 213 9 X 4 AA REPEATS OF P-A-P-A  
FT DOMAIN 156 159 1  
FT REPEAT 160 163 2  
FT REPEAT 180 183 3  
FT REPEAT 184 187 4  
FT REPEAT 188 191 5  
FT REPEAT 198 201 6  
FT REPEAT 202 205 7  
FT REPEAT 206 209 8  
FT REPEAT 210 213 9  
FT DOMAIN 218 281  
FT VARSPLIC 1 11  
FT VARIANT 171 174  
/FTID=VAR\_001404

FT VARIANT 181 184 MISSING (IN HEPATOCELLULAR CARCINOMAS).  
FT FTID=VAR\_001405.  
FT VARIANT 200 203 MISSING (IN A BLADDER CANCER).  
FT FTID=VAR\_001406.  
FT VARIANT 206 209 MISSING (IN A BLAST CANCER).  
FT FTID=VAR\_001407.  
SV SEQUENCE 316 AA; 32177 MW; A94054F06F6B44 C7C664;  
Query Match 18.7%; Score 196.5; DB 1; Length 316;  
Best Local Similarity 22.5%; pred. No. 1,3e-08;  
Matches 71, Conservative 40, Mismatches 77, Indels 127, Gaps 12;  
QY 1 MSNVRVNSGSPSLEPMALPQAIHP---KPSACPMLEFVNVHFEITKRIKHPMPKPSAQ 57  
DB 1 MSDASLSTST-TMERLVAR-GTFPVIVRTSACSLTQPVDFEISRLQARLAEIWAEDQ 58  
QY 58 PKMNPDEGNKHPVLT---GVYEWQVFEKSTIPPEYVYV-----PPPPKSAVYV--- 101  
DB 59 NPMVYDQGLMPLMPLMPLMPLMPLMPLMPLMPLMPLMPLMPLMPLMPLMPLMPLMPL 118  
QY 102 LAGEQVNSNSQV-----VPIQSQANSEDRHIV----- 141  
DB 119 LEPAESLDGLEAPLEQIPSVVPAPASTPEPVPLAFAFAFAFAFAFAFAFAFAFAFAFA 178  
QY 132 -----DMPDSSINQAG-----L 144  
DB 179 AFAT 248  
QY 145 AEGC-PGMKRPKPAEDSSQ-----NKPANRIENSD----- 176  
DB 249 AAGVHSISLSYAPATATAAVAVNAIAIKIISVHIAVAVVAVVAVVAVVAVVAVVAVV 298  
QY 177 -GSPNAGVECTPK 190  
DB 299 SAAPGVGSVPTQTPRK 313  
RESULT 8  
CDN1\_MOUSE STANDARD: PRT: 159 AA.  
ID CDN1\_MOUSE  
AC P39689;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cyclin-dependent kinase inhibitor 1 (p21) (CDK-interacting protein 1)  
DE (Melanoma differentiation associated protein).  
CN CDKN1A OR CIP1 OR WAF1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=BXSB; TISSUE=Spleen;  
RX MEDLINE=94366751; PubMed=8084607;  
RA Huppi K., Siwarski D., Dosik J., Mitchell P., Chedid M., Reed S.,  
RA Mock R., Givol D., Mushinski J.F.;  
RT "Molecular cloning, sequencing, chromosomal localization and  
expression of mouse p21 (Waf1).";  
RT Oncogene 9:5017-5026(1994).  
RN (2)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95316868; PubMed=7796420;  
RA El-Deiry W.S., Tokino T., Waldman T., Velculescu V., Jin J.D.,  
RA Burrell M., Hill D.P., Rees J.L., Hamilton S.R., Kinzler K.W.,  
RA Vogelstein B.;  
RT "Topological control of p21WAF1/CIP1 expression in normal and  
neoplastic tissues.";  
RT Cancer Res. 55:2910-2919(1995).  
RN (3)  
RP SEQUENCE OF 1-143 FROM N.A.  
RX MEDLINE=94061997; PubMed=8242752;  
RA El-Deiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons K.,













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OM protein - protein search, using SW mode!

Run on May 30, 2003, 08:53:57, Search time: 34 sec, Sequences (without alignments) 1181.337 Million cell updates/sec

Title: US-09-865-018b-4

Perfect score: 1051

Sequence: 1 MSNVRVNSGSPLEKMRPAP... SPNACTVQPTKKKRIKPT 197

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_rhiz:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1012	96.3	197	11	U08769 ratius norv
2	1007	95.8	197	11	035792 ratius norv
3	928	88.3	198	4	096TE0
4	927	88.2	198	6	09BDC3
5	925	88.0	198	4	09BYG6
6	924	87.9	198	4	09BUC6
7	740	70.4	158	4	043806
8	730	69.5	172	6	09BEA5
9	355	33.8	179	13	090YX4
10	220	20.9	210	13	091603
11	216	20.6	42	11	090XK6
12	214	20.4	335	11	091V06
13	212	20.2	209	11	091V45
14	190	18.1	42	4	090H60
15	182	17.3	164	11	064315
16	164	15.6	164	4	096LE1

17	162	15.4	181	4	014010
18	141.5	13.5	238	5	022198
19	144	12.7	259	5	0900P5
20	120.5	11.5	253	5	09M002
21	117	11.1	184	5	022197
22	109.5	10.4	245	5	094536
23	109	10.4	255	5	091654
24	107.5	10.2	235	5	191602
25	104	9.4	579	5	095XW4
26	103	9.8	191	10	004154
27	103	9.8	191	10	082809
28	101.5	9.7	1008	10	09M004
29	95	9.1	1277	11	035821
30	95.5	9.1	1277	11	093V92
31	95.5	9.1	570	16	097F01
32	95.5	9.1	630	5	09M433
33	94.5	9.0	643	4	09N0E0
34	94.5	9.0	1045	5	015852
35	94.5	9.0	1211	11	035233
36	93	8.8	437	4	096012
37	93	8.8	2063	4	096FE2
38	92.5	8.8	294	5	020304
39	92.5	8.8	294	5	020304
40	92	8.8	303	10	09EYB1
41	92	8.8	437	10	094C48
42	91.5	8.7	528	4	095238
43	91.5	8.7	737	4	09M002
44	91.5	8.7	738	4	09M002
45	91.5	8.7	748	4	090B30

## ALIGNMENTS

### RESULT 1

U08769 PRELIMINARY: PRT: 197 AA.

AC 008769:

DT 01-JUL-1997 (TREMBL:U08769.04, Created)

DT 01-JUL-1997 (TREMBL:U08769.04, Last sequence update)

DT 01-DEC-2001 (TREMBL:U08769.19, Last annotation update)

DE P27 K1P1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.

NCBI\_TaxID=10116;

OX

RN

RN

RP

RP

RA

RA

RL

RL

RN

RN

RP

RP

RA

RA

RL

RL

RN

RN

RP

RP

RA

RA

RL

RL

RN

RN

RP

RP

RA

014010 homo sapien  
022198 caenorhabd  
0900P5 caenorhabd  
09M002 drosophila  
022197 caenorhabd  
094536 drosophila  
091654 drosophila  
191602 drosophila  
095XW4 caenorhabd  
004154 arabidopsis  
082809 arabidopsis  
09M004 arabidopsis  
035821 rattus norv  
093V92 nitrocladia  
097F01 drosophila  
09M433 drosophila  
09N0E0 homo sapien  
015852 plasmodium  
035233 mus musculu  
096012 homo sapien  
096FE2 homo sapien  
020304 caenorhabd  
020304 caenorhabd  
09EYB1 arabidopsis  
094C48 arabidopsis  
095238 homo sapien  
09M002 homo sapien  
09M002 homo sapien  
090B30 homo sapien

Query Match: 96.3% Score 1012 DB 11 Length 197;  
Fast local similarity 96.4% Pred. No. 197-81;  
Matches 190; Conservative 2; Mismatches 5; Indels 0; Gaps 0;



DB 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVLAQSDVDVSGSRQAVPLIG 120  
 QY 121 SQANSEDRHLVDQMFDSSDQAGLAEGCAGTMMKPPAAAEISSQNKPRANPTEENVSDSSPN 189  
 DB 121 SQANSEDRHLVDQKIDAEUSUGLAEGCAGTMMKPPAAAEISSQNKPRANPTEENVSDSSPN 189  
 QY 181 AGTVEQTPKKPGLRRQ 196  
 DB 181 SASVEQTPKKPGLRRR 196

## RESULT 5

Q9NYG6 PRELIMINARY: PRT: 198 AA.

AC Q9NYG6: 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Cyclin-dependent kinase inhibitor p27kip1.  
 OS Homo sapiens (Human).  
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,  
 OC Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HEPATOMA;  
 RA Li J., Wang W.-L., Yang X.-K., Yu X.-X.;  
 RT "Homo sapiens cyclin-dependent kinase inhibitor p27kip1 cDNA."  
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF247551; AAF69497.1; -;  
 DR InterPro: IPR003175; CDI.  
 DR Pfam: PF02234; CDI; 1.  
 KW kinase.

SQ SEQUENCE 198 AA: 42039 MW: 40670564100PFEA GRG64.

Query Match 88.0%, Score 925, DB 4, length 198;  
 Best local Similarity 87.2%; Pred. No. 8, 5e 74,  
 Matches 171; Conservative 11; Mismatches 14; Indels 0; Gaps 0.

QY 1 MSNVVNSGSPSLPEFMADRAQADHPKPSACRNIFGVNHEELTRDLFKHCRDMEASQPKW 60  
 DB 1 MSNVVNSGSPSLPEFMADRAQADHPKPSACRNIFGVNHEELTRDLFKHCRDMEASQPKW 60  
 QY 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVLAQSDVDVSGSRQAVPLIG 120  
 DB 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVLAQSDVDVSGSRQAVPLIG 120  
 QY 121 SQANSEDRHLVDQMFDSSDQAGLAEGCAGTMMKPPAAAEISSQNKPRANPTEENVSDSSPN 180  
 DB 121 SQANSEDRHLVDQKIDAEUSUGLAEGCAGTMMKPPAAAEISSQNKPRANPTEENVSDSSPN 180  
 QY 181 AGTVEQTPKKPGLRRQ 196  
 DB 181 AGTVEQTPKKPGLRRR 196

## RESULT 6

Q9BUS6 PRELIMINARY: PRT: 198 AA.

AC Q9BUS6: 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Similar to cyclin-dependent kinase inhibitor 1b (p27, kip1).  
 OS Homo sapiens (Human).  
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,  
 OC Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=CERVIX;  
 RA Strausberg R.;  
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.

DB 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVLAQSDVDVSGSRQAVPLIG 120  
 QY 121 SQANSEDRHLVDQMFDSSDQAGLAEGCAGTMMKPPAAAEISSQNKPRANPTEENVSDSSPN 180  
 DB 121 SQANSEDRHLVDQKIDAEUSUGLAEGCAGTMMKPPAAAEISSQNKPRANPTEENVSDSSPN 180  
 QY 181 AGTVEQTPKKPGLRRQ 196  
 DB 181 AGTVEQTPKKPGLRRR 196

Query Match 87.9%, Score 924, DB 4, length 198;  
 Best local Similarity 86.1%; Pred. No. 1, 2e-57;  
 Matches 171; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

## RESULT 7

Q43806 PRELIMINARY: PRT: 158 AA.

AC Q43806: 01-JUN-1998 (TREMblrel. 06, Created)  
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE p27 kip1 protein (Fragment).  
 CN p27 kip1.  
 OS Homo sapiens (Human).  
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,  
 OC Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BREAST CARCINOMA;  
 RX MEDLINE=9614077; PubMed=8557269;  
 RA Ferrando A.A., Balbin M., Pendas A.M., Vizoso F., Velasco G.,  
 RA Lopez-Otin C.;  
 RT "Mutational analysis of the human cyclin-dependent kinase inhibitor  
 p27 kip1 in primary breast carcinomas."  
 RL Hum. Genet. 97:91-94(1996).  
 DR EMBL: X84849; CAA59284.1; -;  
 DR InterPro: IPR003175; CDI.  
 DR Pfam: PF02234; CDI; 1.  
 FT VARIANT 109 109 G -> V.  
 FT NON-TER 158 158  
 SO SEQUENCE 158 AA: 17651 MW: 18627905822PNT50 GRG64;

Query Match 70.4%, Score 740, DB 4, length 158;  
 Best local Similarity 86.1%; Pred. No. 1, 2e-57;  
 Matches 136; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MSNVVNSGSPSLPEFMADRAQADHPKPSACRNIFGVNHEELTRDLFKHCRDMEASQPKW 60  
 DB 1 MSNVVNSGSPSLPEFMADRAQADHPKPSACRNIFGVNHEELTRDLFKHCRDMEASQPKW 60  
 QY 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVLAQSDVDVSGSRQAVPLIG 120  
 DB 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVLAQSDVDVSGSRQAVPLIG 120  
 QY 121 SQANSEDRHLVDQMFDSSDQAGLAEGCAGTMMKPPAAAEISSQNKPRANPTEENVSDSSPN 180  
 DB 121 SQANSEDRHLVDQKIDAEUSUGLAEGCAGTMMKPPAAAEISSQNKPRANPTEENVSDSSPN 180





OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NCRL; TISSUE=PROSTATE.  
RT Wally D., Loda M.;  
RA "Rat cyclin-dependent kinase inhibitor p27 intron";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF213701; AAF21059.1; -.  
KW Kinase.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 42 AA: 4489 MW: 92476255FC3F86C GPC64,  
Query Match 20.6%, Score 215; DB 11; Length 42;  
Best Local Similarity 100.0%; Pred. No. 3e-12;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 144 LAECGPMRKPRAEDSSONKRRANTEENVSQSGSPNAGTVE 185  
DB 1 LAECGPMRKPRAEDSSONKRRANTEENVSQSGSPNAGTVE 42  
RESULT 12  
Q91V06 PRELIMINARY: PRT; 335 AA.  
AC Q91V06.  
DT 01-DEC-2001 (TREMURel. 19, Created)  
DT 01-DEC-2001 (TREMURel. 19, last sequence update)  
DT 01-JUN-2002 (TREMURel. 21, last annotation update)  
DE Cyclin-dependent kinase inhibitor 1C (P57KIP2 protein) (P57)  
GN CNK1C OR P57KIP2.  
OS Mus musculus domesticus (western European house mouse); and  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
OC NCBI\_TaxID=10092, 10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Mus musculus domesticus; STRAIN=129 SV;  
RX MEDLINE=20519229; PubMed=11063728;  
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt P.,  
LA Lane N., Reik W., Walter J.;  
RT "Sequence and functional comparison in the Beckwith-Wiedemann region;  
RT implications for a novel imprinting centre and extended imprinting";  
RL Hum. Mol. Genet. 9:2691-2706(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Mus musculus domesticus; STRAIN=129 SV;  
RA Engemann S.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Mouse; STRAIN=129/SV;  
RX MEDLINE=20014712; PubMed=10545601;  
RA John P.M., Hodges M., Little P., Barton S.C., Surani M.A.;  
RT "A human p57KIP2 transgene is not activated by passage through the  
RT maternal mouse germline.";  
RL Hum. Mol. Genet. 8:2211-2219(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Mouse; TISSUE=BREAST TUMOR;  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases  
DR EMBL: AJ276505; CAC16402.1; -.  
DR EMBL: AF160130; AAF00983.1; -.  
DR EMBL: BC005412; AA05412.1; -.  
DR MGD: MG1:104564; Cdkn1c.  
DR InterPro: IPR003175; CDI.  
DR Pfam: PF02234; CDI; 1.  
KW Kinase.  
SQ SEQUENCE 335 AA: 35903 MW: 55040675287FEB3F CRC64;  
Query Match 20.4%; Score 214; DB 11; Length 335,

Best Local Similarity 10.0%; Pred. No. 6e-11;  
Matches 57; Conservative 28; Mismatches 67; Indels 38; Gaps 6;  
QY 25 KLSAIVNPLDYNHETLTLKKEKMPFASQPYWNPQNHKPIF-LGYWCVVPP- 92  
DB 15 FSSACFSGFVGFHFFGFIEMFLATNATGKMFNFGVPIKPPRIUMEDSE 74  
QY 83 SLPEFYTP-----PPPKSCKVLAGEQVSGPQAVPLIGSQANSEIRILY 131  
DB 75 SVPAFYKEIVGVGCPQLDGPFPVAVV-----IPSGPAPADGLE 120  
QY 132 E--GMPSSLDQALAECCPMRKPRAEDSSONKRR-----ANPTEENVSGSPNAGT 183  
DB 121 EAPGHTSARASAVVAERTPATPAVASDLISDFEVLVAISDFEILQANLVAI 180  
QY 184 ---VEQTPKK 190  
DB 181 RDGEQVPEQ 190  
RESULT 13  
Q91646 PRELIMINARY: PRT; 209 AA.  
AC Q91646.  
DT 01-NOV-1996 (TREMURel. 01, Created)  
DT 01-NOV-1996 (TREMURel. 01, last sequence update)  
DT 01-DEC-2001 (TREMURel. 19, last annotation update)  
DE Cyclin-dependent kinase inhibitor p28.  
GN Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OC NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97022113; PubMed=8868473;  
RA Shou W., Dunphy W.G.;  
RT "Cell cycle control by Xenopus p28Kix1, a developmentally regulated  
RT inhibitor of cyclin-dependent kinases";  
RL Mol. Biol. Cell 7:457-469(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Shou W., Dunphy W.G.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U38644; AAC59775.1; -.  
DR InterPro: IPR003175; CDI.  
DR Pfam: PF02234; CDI; 1.  
KW Kinase.  
SQ SEQUENCE 209 AA: 23475 MW: 45940447540C6 GRC64;  
Query Match 20.2%; Score 212; DB 13; Length 209;  
Best Local Similarity 26.0%; Pred. No. 5e-11;  
Matches 54; Conservative 39; Mismatches 73; Indels 42; Gaps 5;  
QY 14 ERMDARQADHFKS-----ACNLTGFVMIHETLQLEHCHQXDEFASQKNTFFQNH 67  
DB 10 EEMISAVAVLPKLSAGISGACNKLHGFIIHDEMSLAKQLKEIQAISDQUPNNPFETG 69  
QY 68 KLECFYMECEVEFGESLPEFYF-----FEFTFSACFVAGTSGQVSGSPQAVPI 119  
DB 70 TPLKGIQWPEPVPEPKMPSPYSQNPSTANNTSP-----KGGQPIVSGQPEP 118  
QY 120 QSNASHLPHIVLWMPHSTNCAVAPLWMPKPPVAAVSSQANPAPTPVNSGSG 179  
DB 119 HFAFAPVIVENVNIPDAKFNAEKTVKFGVGVWQSPASANTSTGPKKFTITITVPL 178  
QY 180 NAGTV-----RQTPKK 190  
DB 179 KKKKILSAKPAIKGAHLCLCPDQTPKK 206  
RESULT 14  
Q9UH60

ID GENEID PDBLIMNARY: PR1: 42 AA.  
 AC GENEID:  
 DT 01 MAY 2003 (GEMMID01: 15, created)  
 DT 01 MAY 2003 (GEMMID01: 15, last sequence update)  
 DT 01 DEC 2001 (GEMMID01: 19, last annotation update)  
 DE cyclin dependent kinase inhibitor p27 (Protein).  
 OS Homo sapiens (human).  
 CC Fokuyama M (1999), Characterization of a novel cyclin dependent kinase inhibitor, p27, from human.  
 CC Mammalian Pathology, Chromatin Architecture, Hematology, Hematology, Hematology.  
 CC NCBI TaxID 9606.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Wallingford D, Loda M.  
 RT "Homo sapiens cyclin dependent kinase inhibitor p27 (human)".  
 RL Submitted (DEC 1999) to the EMBL/GenBank/CCDS databases.  
 DR EMBL: AF217079; AACL109411.  
 KW Kinase.  
 FT NON TER 1  
 FT NON TER 42  
 SO SEQUENCE 42 AA; 4461 MW; 9285/4982/5967/9 (60%AA).

Query Match ID: 144 Score: 1907 DB: 4; Length: 427  
 Host Local Similarity: 85.7%; Prot. No.: 5, 80, 10; Labels: 6; Pairs: 2  
 Matches: 46; Conserved: 4; Mismatches: 2; Indels: 0  
 Y 144 LAFQYEMRQVAMRSGSRKAKRRTERRVSRNSNATVE 195  
 1 LAFQVALLRFATLSSITGRKAKRRTERRVSRNSNATVE 42

RESULT 15  
 ID G64415 PDBLIMNARY: PR1: 164 AA.  
 AC G64415:  
 DT 01 NOV 1996 (GEMMID01: 01, created)  
 DT 01 NOV 1996 (GEMMID01: 01, last sequence update)  
 DT 01 DEC 2001 (GEMMID01: 19, last annotation update)  
 DE P21 (WAF1).  
 CN WAF1 (WAF1).  
 CC Ratios: 100% (WAF1).  
 CC Fokuyama M (1999), Characterization of a novel cyclin dependent kinase inhibitor, p27, from human.  
 CC Mammalian Pathology, Chromatin Architecture, Hematology, Hematology, Hematology.  
 CC NCBI TaxID 10116.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 9641600; PMID: 7704200  
 RA of Isely W, St. John L, Waldman T, Wolfenson V, Fisher J, Lee RA, Bortell M, Hill D, Ross J, Lee Hamilton S, R. Kinzler K.W.  
 RA Vogelstein B.  
 RT "Topological control of p21(WAF1/CIP1) expression in normal and neoplast cells".  
 RT Cancer Res. 59:291-294 (1999).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA STRAIN F44/N; FIS06 LUNG;  
 RA BOLLINSKY S.A.  
 RL Submitted (MAY 1993) to the EMBL/GenBank/CCDS databases.  
 DR EMBL: U24174; AAC122111.  
 DR EMBL: U24175; AAC1208411.  
 DR InfoProc: 19900417; C01.  
 DR InfoProc: 1990244; C01.  
 SO SEQUENCE 164 AA; 18416 MW; 607/5904/1064/9 (60%AA).

Query Match ID: 174 Score: 1067 DB: 11; Length: 164  
 Host Local Similarity: 26.8%; Prot. No.: 1, 60, 06; Labels: 2; Pairs: 4  
 Matches: 46; Conserved: 2; Mismatches: 6; Indels: 0

Y 17 LAFQYEMRQVAMRSGSRKAKRRTERRVSRNSNATVE 195  
 1 LAFQVALLRFATLSSITGRKAKRRTERRVSRNSNATVE 42  
 Y 17 LAFQYEMRQVAMRSGSRKAKRRTERRVSRNSNATVE 195  
 1 LAFQVALLRFATLSSITGRKAKRRTERRVSRNSNATVE 42

ID G64415 PDBLIMNARY: PR1: 164 AA.  
 AC G64415:  
 DT 01 NOV 1996 (GEMMID01: 01, created)  
 DT 01 NOV 1996 (GEMMID01: 01, last sequence update)  
 DT 01 DEC 2001 (GEMMID01: 19, last annotation update)  
 DE P21 (WAF1).  
 CN WAF1 (WAF1).  
 CC Ratios: 100% (WAF1).  
 CC Fokuyama M (1999), Characterization of a novel cyclin dependent kinase inhibitor, p27, from human.  
 CC Mammalian Pathology, Chromatin Architecture, Hematology, Hematology, Hematology.  
 CC NCBI TaxID 10116.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 9641600; PMID: 7704200  
 RA of Isely W, St. John L, Waldman T, Wolfenson V, Fisher J, Lee RA, Bortell M, Hill D, Ross J, Lee Hamilton S, R. Kinzler K.W.  
 RA Vogelstein B.  
 RT "Topological control of p21(WAF1/CIP1) expression in normal and neoplast cells".  
 RT Cancer Res. 59:291-294 (1999).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA STRAIN F44/N; FIS06 LUNG;  
 RA BOLLINSKY S.A.  
 RL Submitted (MAY 1993) to the EMBL/GenBank/CCDS databases.  
 DR EMBL: U24174; AAC122111.  
 DR EMBL: U24175; AAC1208411.  
 DR InfoProc: 19900417; C01.  
 DR InfoProc: 1990244; C01.  
 SO SEQUENCE 164 AA; 18416 MW; 607/5904/1064/9 (60%AA).

Search completed: May 01, 2003, 09:01:00  
 Job Time: 3:45, 46000 Steps





PT especially breast carcinoma  
 XX  
 PS Disclosure: Fig 14B, 105pp; English.  
 XX  
 CC The present sequence represents a 27 kDa protein (p27 or Kip1) which  
 CC inhibits the activation of a cyclin E-cyclin-dependent kinase2 (Cdk2)  
 CC complex. A reduced relative level of kip1 is indicative of a  
 CC hyperproliferative disease (particularly cancer; especially breast  
 CC carcinoma) and also is prognostic for increased risk of death and/or  
 CC recurrence of cancer (and may be used to determine suitable treatments).  
 CC Agents that affect the activity of kip1 can be used to treat  
 CC hyperproliferative conditions, e.g. to stimulate tissue or organ repair  
 CC or to establish cell cultures.  
 XX  
 SQ Sequence 197 AA;  
 Query Match 100.0%; Score 384; DB 19; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 7,8e-42;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DHPKPSACRNLFPGVNHHELTIDLEKHCRCMEASQKWNFDPNHKPLEGRYEMQEVER 60  
 DB 22 DHPKPSACRNLFPGVNHHELTIDLEKHCRCMEASQKWNFDPNHKPLEGRYEMQEVER 81  
 OY 61 GSLPEFY 67  
 DB 82 GSLPEFY 88  
 Db 82 GSLPEFY 88  
 RESULT 4  
 ID AAY08819  
 AC AAY08819 standard; Protein; 197 AA.  
 XX  
 AC AAY08819;  
 DT 13-AUG-1999 (first entry)  
 DT  
 DE Mouse wild type p27 protein.  
 XX  
 KM Activation sequence; transcription factor, murine, p163, p27, treatment;  
 KM binding protein; DNA binding domain; effector gene; disease; infection;  
 KM tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;  
 KM transplant rejection; graft-versus-host disease; circulatory disorder;  
 KM blood clot; anaemia; hormonal disorder; CNS injury.  
 XX  
 OS Mus sp.  
 XX  
 PN EP926237-A2.  
 XX  
 PD 30-JUN-1999.  
 XX  
 PF 12-DEC-1998; 98EP-0123709.  
 XX  
 PR 20-DEC-1997; 97DE-1056975.  
 XX  
 PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.  
 XX  
 PI Buergin A, Eilers M, Sedlacek H;  
 XX  
 DR WPI: 1999-349237/30.  
 XX  
 PT New nucleic acid construct comprising product, transcription factor  
 PT gene, activation sequence and effector gene - useful for gene  
 PT therapy treatment of allergies, inflammation, transplant disorders  
 PT and leukaemia  
 XX  
 PS Disclosure: Page 49, 90pp, German.  
 XX  
 CC This invention describes a novel nucleic acid construct comprising the  
 CC following components (a) an activation sequence for the transcription  
 CC of component b, (b) component b which is constructed from component b1  
 CC (a transcription factor activating domain), component b2 (murine p163  
 CC or p27 binding protein) and component b3 (a transcription factor DNA

CC binding domain), (c) an activation sequence which is activated by binding  
 CC of the expression product of component (b) and which induces  
 CC transcription of component (d) and (d) an effector gene. The construct,  
 CC preferably in a plasmid or viral vector, or cell can be used to treat a  
 CC disease selected from infections, tumours, leukaemia, autoimmune  
 CC diseases, allergies, arthritis, inflammations, transplant rejection,  
 CC graft-versus-host disease, blood clotting disorders, circulatory  
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence  
 CC represents the murine p27 protein which is used in the method of the  
 CC invention.  
 XX  
 SQ Sequence 197 AA;  
 Query Match 100.0%; Score 384; DB 20; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 7,8e-42;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DHPKPSACRNLFPGVNHHELTIDLEKHCRCMEASQKWNFDPNHKPLEGRYEMQEVER 60  
 DB 22 DHPKPSACRNLFPGVNHHELTIDLEKHCRCMEASQKWNFDPNHKPLEGRYEMQEVER 81  
 OY 61 GSLPEFY 67  
 DB 82 GSLPEFY 88  
 Db 82 GSLPEFY 88  
 RESULT 5  
 ID AAY08847  
 AC AAY08847 standard; Protein; 197 AA.  
 XX  
 AC AAY08847;  
 DT 13-AUG-1999 (first entry)  
 DT  
 DE Murine wild type p27 protein.  
 XX  
 KM p163; murine; p27 inhibitor; p27-induced inhibition; cell proliferation;  
 KM p27 binding domain; Ran binding domain; detection; screening; malignancy;  
 KM tumour; mutant; p27 protein.  
 XX  
 OS Mus sp.  
 XX  
 PN EP926236-A1.  
 XX  
 PD 30-JUN-1999.  
 XX  
 PF 12-DEC-1998; 98EP-0123708.  
 XX  
 PR 20-DEC-1997; 97DE-1056975.  
 XX  
 PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.  
 XX  
 PI Buergin A, Eilers M, Sedlacek H;  
 XX  
 DR WPI: 1999-349237/30.  
 XX  
 PT New p27-inhibiting protein p163 and DNA - useful for detection  
 PT and/or quantification of p163 mRNA  
 XX  
 PS Disclosure: Page 28, 68pp, German.  
 XX  
 CC This invention describes (1) a protein that inhibits p27 and thereby  
 CC arrests p27-induced inhibition of cell proliferation, (2) the protein of  
 CC (1) comprising at least part of the amino acid sequence of murine p163,  
 CC (3) a protein that can be derived from the protein of (2) by deletion of  
 CC the p27 binding domain or the Ran binding domain, (4) a protein that can  
 CC be derived from the protein of (2) by deletion of all amino acid  
 CC sequences other than the p27 binding domain, (5) a protein that is the  
 CC human or other mammalian species homologue of a protein as in (1) (4),  
 CC (6) DNA encoding the p163 protein, (7) antibodies and antibody fragments  
 CC that bind to the p27 binding domain of a protein as above, (8) antibodies  
 CC and antibody fragments that bind to the Ran binding domain of a protein  
 CC as above, (9) antisense nucleic acids complementary to portions of the



CC following components (a) an activation sequence for the transcription  
CC of component b, (b) component b which is constructed from component b1  
CC (a transcription factor activating domain), component b2 (murine p163  
CC or p27 binding protein) and component b3 (a transcription factor DNA  
CC binding domain), (c) an activation sequence which is activated by binding  
CC of the expression product of component (b) and which induces  
CC transcription of component (d) and (d) an effector gene. The construct,  
CC preferably in a plasmid or viral vector, or cell can be used to treat a  
CC disease selected from infections, tumours, leukaemia, autoimmune  
CC diseases, allergies, arthritis, inflammations, transplant rejection,  
CC graft-versus-host disease, blood clotting disorders, circulatory  
CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence  
CC represents a mutant murine p27 protein which is used to describe the  
CC method of the invention.

CC Sequence 138 AA;

Query Match 98.2% Score 377; DB 20; Length 138;

Best Local Similarity 98.5% Pred. No. 4,1e-41; Indels 0; Gaps 0;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPKPSACRNLFGPVNHEELTRDEKHCROMEASQKKNFDFQNHKPLEGRYEMQEVER 60  
DB 7 DHPKPSACRNLFGPVNHEELTRDEKHCROMEASQKKNFDFQNHKPLEGRYEMQEVER 66  
QY 61 GSLEPEFY 67  
DB 67 GSLEPEFY 73

De

AA08846

AA08846 standard; Protein; 138 AA.

DT 13-AUG-1999 (first entry)

XX Murine mutant p27 protein from clone #850.

KW p163; murine; p27 inhibitor, p27-induced inhibition; cell proliferation;  
KM p27 binding domain; Ran binding domain; detection; screening; malignancy;  
KM tumour; mutant; p27 protein.

OS Mus sp.

PN EP926236-A1.

XX 30-JUN-1999.

XX 12-DEC-1998; 98EP-0123708.

XX 20-DEC-1997; 97DE-1056975.

XX (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

PI Buerquin A, Eilers M, Sedlacek H;

DR WPI; 1999-349237/30.

PT New p27-inhibiting protein p163 and DNA - useful for detection  
PT and/or quantification of p163 mRNA

PS Disclosure; Page 28; 68pp; German.

XX This invention describes (1) a protein that inhibits p27 and thereby  
CC arrests p27-induced inhibition of cell proliferation, (2) the protein of  
CC (1) comprising at least part of the amino acid sequence of murine p163  
CC (3) a protein that can be derived from the protein of (2) by deletion of  
CC the p27 binding domain or the Ran binding domain, (4) a protein that can  
CC be derived from the protein of (2) by deletion of all amino acid  
CC sequences other than the p27 binding domain, (5) a protein that is the  
CC human or other mammalian species homologue of a protein as in (1)-(4).

CC (6) RNA encoding the p163 protein, (7) antibodies and antibody fragments  
CC that bind to the p27 binding domain of a protein as above, (8) antibodies  
CC and antibody fragments that bind to the Ran binding domain of a protein  
CC as above, (9) antisense nucleic acids complementary to portions of the  
CC RNA of (6) between codons 121 and 467, (10) a nucleic acid construct  
CC coding for an antisense nucleic acid as in (9) for inhibiting the  
CC proliferation of a cell, in which DNA coding for the antisense nucleic  
CC acid sequence is linked to at least one activation sequence and is  
CC introduced into the target cell as naked DNA or as an insert in a  
CC vector of viral vector and (11) a nucleic acid construct containing the  
CC RNA of (6) linked to an activation sequence that permits expression of a  
CC protein as above in a cell. The RNA of (6) can be used for detection  
CC and/or quantification of p163 mRNA in cells and/or tissues. Preferably by  
CC Northern blotting, PCR or fluorescent in-situ hybridisation. The proteins  
CC can be used to produce antibodies which can be used to detect the  
CC corresponding protein in cells, tissues or body fluids. The antisense  
CC nucleic acids can be used to inhibit cell proliferation in vitro or in  
CC vivo. The proteins can be used to screen for substances that inhibit the  
CC interaction between the proteins and the intracellular binding partners,  
CC preferably using a two hybrid system or using an affinity system in which  
CC p163 or its p27-binding domain is immobilised on a solid phase, the solid  
CC phase is incubated with a test substance, and the inhibition of the  
CC binding of a labelled binding partner of p163 (especially p27 or Ran) is  
CC measured. Assays for p163 can be used to assess the malignancy of  
CC tumours. This sequence represents a mutant mouse p27 protein sequence  
CC isolated from clone #826 which is used to describe the method of the  
CC invention.

SO Sequence 138 AA;

Query Match 98.2% Score 377; DB 20; Length 138;

Best Local Similarity 98.5% Pred. No. 4,1e-41; Indels 0; Gaps 0;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPKPSACRNLFGPVNHEELTRDEKHCROMEASQKKNFDFQNHKPLEGRYEMQEVER 60  
DB 7 DHPKPSACRNLFGPVNHEELTRDEKHCROMEASQKKNFDFQNHKPLEGRYEMQEVER 66

QY 61 GSLEPEFY 67

DB 67 GSLEPEFY 73

De

AA08812

AA08812 standard; Protein; 183 AA.

XX 30-JUN-1999.

XX 13-AUG-1999 (first entry)

XX Mouse p27 mutant protein 1.

KW Activation sequence; transcription factor; murine; p163; p27; treatment;  
KM binding protein; DNA binding domain; effector gene; disease; infection;  
KM tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;  
KM transplant rejection; graft-versus-host disease; circulatory disorder;  
KM blood clot; anaemia; hormonal disorder; CNS injury; mutant.

OS Mus sp.

PN EP926237 A2.

XX 30-JUN-1999.

XX 12-DEC-1998; 98EP-0123709.

XX 20-DEC-1997; 97DE-1056975.

XX (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

PI Buerquin A, Eilers M, Sedlacek H;

DR WPI; 1999-349237/30.

PT New p27-inhibiting protein p163 and DNA - useful for detection  
PT and/or quantification of p163 mRNA

PS Disclosure; Page 28; 68pp; German.





PD 30-JUN-1999.  
 XX  
 XX 12-DEC-1998; 98EP-0123709.  
 PF  
 XX 20-DEC-1997; 97DE-1056975.  
 PR  
 XX (HMRI ) HOECHST MARTON ROUSSEL DEUT GMBH.  
 PA  
 XX Buergin A, Eilers M, Sedlacek H;  
 PI  
 XX WPI: 1999-349238/30.  
 DK  
 XX  
 PT New nucleic acid construct comprising promoter, transcription factor  
 PT gene, activation sequence and effector gene - useful for gene  
 PT therapy treatment of allergies, inflammation, transplant disorders  
 PT and leukaemia  
 PS  
 XX Disclosure; Page 49; 90pp; German.  
 CC  
 XX This invention describes a novel nucleic acid construct comprising the  
 CC following components (a) an activation sequence for the transcription  
 CC of component b, (b) component b which is constructed from component b1  
 CC (a transcription factor activating domain), component b2 (murine p163  
 CC or p27 binding protein) and component b3 (a transcription factor DNA  
 CC binding domain), (c) an activation sequence which is activated by binding  
 CC of the expression product of component (b) and which induces  
 CC transcription of component (d) and (d) an effector gene. The construct,  
 CC preferably in a plasmid or viral vector, or cell can be used to treat a  
 CC disease selected from infections, tumours, leukaemia, autoimmune  
 CC diseases, allergies, arthritis, inflammations, transplant rejection,  
 CC graft-versus-host disease, blood clotting disorders, circulatory  
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence  
 CC represents a mutant murine p27 protein which is used to describe the  
 CC method of the invention.  
 CC  
 XX  
 SQ Sequence 199 AA;  
 Query Match 98.2%; Score 377; DB 20; Length 199;  
 Best Local Similarity 98.5%; Pred. No. 6,5e-41;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DHPKPSACRNLFGPVNHEELTPLEKHKRMPEASQPKWNFPQNHKPLGSPYFWQPYEP 60  
 DB 18 DHPKPSACRNLFGPVNHEELTPLEKHKRMPEASQPKWNFPQNHKPLGSPYFWQPYEP 77  
 QY 61 GSLPEFY 67  
 DB 78 GSLPEFY 84  
 RESULT 12  
 ID AAY08815  
 ID AAY08815 standard; Protein: 199 AA.  
 AC AAY08815;  
 XX  
 DT 13-AUG-1999 (first entry)  
 DE  
 XX Mouse p27 mutant protein 4.  
 DE  
 XX  
 KM Activation sequence; transcription factor; murine; p163; p27; treatment;  
 KM binding protein; DNA binding domain; effector gene; disease; infection;  
 KM tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;  
 KM transplant rejection; graft-versus-host disease; circulatory disorder;  
 KM blood clot; anaemia; hormonal disorder; CNS injury; mutant.  
 XX  
 OS Mus sp.  
 XX  
 PN EP926237-A2.  
 XX  
 PD 30-JUN-1999.  
 PD  
 XX 12-DEC-1998; 98EP-0123709.  
 PF

XX  
 PR 20-DEC-1997; 97DE-1056975.  
 PA  
 XX (HMRI ) HOECHST MARTON ROUSSEL DEUT GMBH.  
 XX  
 PI Buergin A, Eilers M, Sedlacek H;  
 XX  
 DR WPI: 1999-349238/30.  
 XX  
 PT New nucleic acid construct comprising promoter, transcription factor  
 PT gene, activation sequence and effector gene - useful for gene  
 PT therapy treatment of allergies, inflammation, transplant disorders  
 PT and leukaemia  
 PS  
 XX Disclosure; Page 49; 90pp; German.  
 CC  
 XX This invention describes a novel nucleic acid construct comprising the  
 CC following components (a) an activation sequence for the transcription  
 CC of component b, (b) component b which is constructed from component b1  
 CC (a transcription factor activating domain), component b2 (murine p163  
 CC or p27 binding protein) and component b3 (a transcription factor DNA  
 CC binding domain), (c) an activation sequence which is activated by binding  
 CC of the expression product of component (b) and which induces  
 CC transcription of component (d) and (d) an effector gene. The construct,  
 CC preferably in a plasmid or viral vector, or cell can be used to treat a  
 CC disease selected from infections, tumours, leukaemia, autoimmune  
 CC diseases, allergies, arthritis, inflammations, transplant rejection,  
 CC graft-versus-host disease, blood clotting disorders, circulatory  
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence  
 CC represents a mutant murine p27 protein which is used to describe the  
 CC method of the invention.  
 CC  
 XX  
 SQ Sequence 199 AA;  
 Query Match 98.2%; Score 377; DB 20; Length 199;  
 Best Local Similarity 98.5%; Pred. No. 6,5e-41;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DHPKPSACRNLFGPVNHEELTPLEKHKRMPEASQPKWNFPQNHKPLGSPYFWQPYEP 60  
 DB 17 DHPKPSACRNLFGPVNHEELTPLEKHKRMPEASQPKWNFPQNHKPLGSPYFWQPYEP 76  
 QY 61 GSLPEFY 67  
 DB 77 GSLPEFY 83  
 RESULT 13  
 ID AAY08843  
 ID AAY08843 standard; Protein: 199 AA.  
 AC AAY08843;  
 XX  
 DT 13-AUG-1999 (first entry)  
 DE  
 XX Murine mutant p27 protein from clone #660.  
 DE  
 XX p163, murine; p27 inhibitor; p27 induced inhibition; cell proliferation;  
 KM p27 binding domain; Ran binding domain; detection; screening; malignancy;  
 KM tumour; mutant; p27 protein.  
 XX  
 OS Mus sp.  
 XX  
 PN EP926236-A1.  
 XX  
 PD 30-JUN-1999.  
 PD  
 XX 12-DEC-1998; 98EP-0123708.  
 PF  
 XX 20-DEC-1997; 97DE-1056975.  
 PD  
 XX  
 PA (HMRI ) HOECHST MARTON ROUSSEL DEUT GMBH.



## RESULT 15

AY08811 TD 2211

ID	AY08811	standard; Protein; 212 AA.
xy		

AC AAY08811;

DT 13-AUG-1999 (first entry)

Mouse p27 protein consensus sequence.

KW Active on sequence: transcription factor; murine; p163; p27; treatment;  
KW binding protein; DNA binding domain; effector gene; disease; infection;  
KW leukaemia; autoimmune disease; allergy; arthritis; inflammation;  
KW transplant rejection; graft-versus-host disease; circulatory disorder;  
KW blood clot; anaemia; normal disorder; CNS injury.

Mus sp.

PN EP926237-A2.

PD 30-JUN-1999.

PF 12-DEC-1998; 98EP-0123709.

PR 20-DEC-1997; 97DE-1056975.

PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

PI Buergin A, Eilers M, Sedlacek H;

DR WPI; 1999-349238/30.

PT New nucleic acid construct comprising promoter, transcription factor gene, activation sequence and effector gene - useful for gene therapy treatment of allergies, inflammation, transplant disorders and leukaemia

PS Disclosure; Page 49; 90pp; German.

Disclosure: Page 49; 90pp; German.

This invention describes a novel nucleic acid construct comprising the following components (a) an activation sequence for the transcription of component b, (b) component b which is constructed from component b1 (a transcription factor activating domain), component b2 (murine p163 or p27 binding protein) and component b3 (a transcription factor DNA binding domain), (c) an activation sequence which is activated by binding of the expression product of component (b) and which induces transcription of component (d) and (d) an effector gene. The construct, preferably in a plasmid or viral vector, or cell can be used to treat a disease selected from infections, tumours, leukaemia, autoimmune diseases, allergies, arthritis, inflammations, transplant rejection, graft-versus-host disease, blood clotting disorders, circulatory disorders, anaemia, hormonal disorders and CNS injuries. This sequence represents the murine p27 protein consensus sequence which is used to describe the method of the invention.

Sequence 212 AA;

	Query Match	Score	DB	Length
	98.2%	377	20	212

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1 DHPKSA <del>C</del> RNLGPGVNHFEI,TKOLEKH,KIMEFAS,QKKNNPUPQNHKLPLESYEWLVEVER 60
Db	18 DHPKSA <del>C</del> RNLGPGVNHGEI,TRDI,EKH,RDMFASQKKNMFQNHKLPLESRYEWELEVER 77

18 DHPKPSACRNI,FGPVNHGEI,TRDI,FKHC,RDMFEASQPRKWN,EDFQNHKPLEGRYEWQEVER. 77

QY 61 GSLPEFY 67

Db 78 GSLEPY 84

Search completed: May 30, 2003, 08:58:26  
Job time : 15.7158 secs

Job time : 15.7158 secs

•

•

GenCute version 5.1.6  
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# OM protein - protein search, using SW model

Run on May 30, 2003, 08:55:37, Search time: 5.02007 seconds  
(without alignments)  
392.644 Million cell updates/sec

Title: US-09-865-018B-4\_COPY\_22\_88  
Sequence: 1 DHPKPSACRNLEGPVNHEEL.....PLEGPTWQVFPSPSPPEFY 67  
Perfect score: 384

Scoring table: RIGSIM62  
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents\_A1:  
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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
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6: /cgn2\_6/ptodata/1/1aa/Backfilest.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	100.0	197	US-08-275-983B-2	Sequence 2, Appl
2	384	100.0	197	US-09-240-906-B	Sequence 8, Appl
3	384	100.0	197	US-09-215-221-57	Sequence 57, Appl
4	384	100.0	197	US-08-794-002-4	Sequence 4, Appl
5	384	100.0	197	US-08-854-039B-4	Sequence 4, Appl
6	379	98.7	197	US-08-415-655-6	Sequence 6, Appl
7	377	98.2	135	US-09-215-221-56	Sequence 56, Appl
8	377	98.2	180	US-09-215-221-50	Sequence 50, Appl
9	377	98.2	193	US-09-215-221-53	Sequence 53, Appl
10	377	98.2	194	US-09-215-221-52	Sequence 52, Appl
11	377	98.2	212	US-09-215-221-49	Sequence 49, Appl
12	373	97.1	180	US-09-215-221-55	Sequence 55, Appl
13	369	96.1	177	US-09-457-568-12	Sequence 12, Appl
14	369	96.1	177	US-09-457-568-12	Sequence 12, Appl
15	369	96.1	194	US-09-215-221-51	Sequence 51, Appl
16	369	96.1	198	US-08-275-983B-3	Sequence 3, Appl
17	369	96.1	198	US-08-406-248-4	Sequence 4, Appl
18	369	96.1	198	US-08-807-333A-2	Sequence 2, Appl
19	369	96.1	198	US-09-240-906-6	Sequence 6, Appl
20	369	96.1	198	US-08-794-002-2	Sequence 2, Appl
21	369	96.1	198	US-09-457-568-26	Sequence 26, Appl
22	369	96.1	198	US-09-457-568-26	Sequence 26, Appl
23	369	96.1	334	US-09-457-568-16	Sequence 16, Appl
24	369	96.1	334	US-09-457-568-16	Sequence 16, Appl
25	369	96.1	348	US-09-457-568-14	Sequence 14, Appl
26	369	96.1	348	US-09-457-568-14	Sequence 14, Appl
27	369	96.1	365	US-09-457-568-6	Sequence 6, Appl

28	369	96.1	365	4	US-09-457-568-10	Sequence 10, Appl
29	369	96.1	365	4	US-09-457-568-6	Sequence 6, Appl
30	369	96.1	365	4	US-09-457-568-10	Sequence 10, Appl
31	369	96.1	380	4	US-09-457-568-8	Sequence 8, Appl
32	369	96.1	380	4	US-09-457-568-8	Sequence 8, Appl
33	369	96.1	391	1	US-08-594-041-2	Sequence 2, Appl
34	369	96.1	391	4	US-09-457-568-4	Sequence 4, Appl
35	369	96.1	391	4	US-09-457-568-4	Sequence 4, Appl
36	361.5	94.1	195	4	US-09-215-221-54	Sequence 54, Appl
37	361	94.0	198	4	US-08-854-039B-2	Sequence 18, Appl
38	359	93.5	80	4	US-09-457-568-18	Sequence 18, Appl
39	359	93.5	80	4	US-09-457-568-18	Sequence 18, Appl
40	359	93.5	237	4	US-09-457-568-20	Sequence 20, Appl
41	359	93.5	237	4	US-09-457-568-20	Sequence 20, Appl
42	359	93.5	252	4	US-09-457-568-22	Sequence 22, Appl
43	359	93.5	252	4	US-09-457-568-22	Sequence 22, Appl
44	356	92.7	178	4	US-08-794-002-6	Sequence 6, Appl
45	356	92.7	178	4	US-08-854-039B-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-08-275-983B-2  
Sequence 2, Application US/08275983B  
Patent No. 568665  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Roberts, James M.  
APPLICANT: Koff, Andrew  
APPLICANT: Polyak, Kornelia  
TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid Molecules  
NUMBER OF SEQUENCES: 19  
FRESH-SEQUENCE ADDRESS:  
ADDRESS: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
ZIP: 02109 1875  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/275,983B  
FILING DATE: 13 SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/174,045  
FILING DATE: 07-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/COCKET NUMBER: MII 079CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO. 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 197 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOIETY/TYPER: peptide  
FRAGMENT TYPE: Internal  
US-08-275-983B 2

Query Match 100.0% Score 384; DB 1; Length 197;  
Host Local Similarity 100.0%; Prev. No. 384-42;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP  
;; STREET: One Post Office Square  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02109-2170  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/854,039B  
;; FILING DATE: 09-MAY-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Vincent, Matthew P.  
;; REGISTRATION NUMBER: 36,709  
;; REFERENCE/DOCKET NUMBER: MIV-079.04  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-832-1000  
;; TELEFAX: 617-832-7000  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 197 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-854-039B-4  
  
Query Match 100.0%; Score 184; DH 4; Length 197;  
Best Local Similarity 100.0%; Pred. No. 2,8e-42;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DHRPSACNLFQGVNHHFLTRDLKRPDMEBASQPKWNPFGNKKPLEGKYVWQVFR 60  
DB 22 DHRPSACNLFQGVNHHFLTRDLKRPDMEBASQPKWNPFGNKKPLEGKYVWQVFR 61  
QY 61 GSLPEFY 67  
DB 82 GSLPEFY 88  
  
RESULT 6  
US-08-415-655-6  
; Sequence 6, Application US/08415655  
; Patent No. 6025480  
; GENERAL INFORMATION:  
; APPLICANT: Massague, Joan  
; APPLICANT: Lee, Mong-hong  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
; TITLE OF INVENTION: p75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF  
; TITLE OF INVENTION: SAME  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/415,655  
; FILING DATE:  
; CLASSIFICATION: 415  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678

;; REFERENCE/DOCKET NUMBER: 1747/47418  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (412) 278-0400  
;; TELEFAX: (412) 391-0525  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 197 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: not relevant  
;; MOLECULE TYPE: protein  
;; HYPOTHEICAL: NO  
;; ANTI-SENSE: NO  
;; US-08-415-655-6  
  
Query Match 98.7%; Score 379; DH 3; Length 197;  
Best Local Similarity 98.5%; Pred. No. 1.2e-41;  
Matches 66; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DHRPSACNLFQGVNHHFLTRDLKRPDMEBASQPKWNPFGNKKPLEGKYVWQVFR 60  
DB 22 DHRPSACNLFQGVNHHFLTRDLKRPDMEBASQPKWNPFGNKKPLEGKYVWQVFR 61  
QY 61 GSLPEFY 67  
DB 82 GSLPEFY 88  
  
RESULT 7  
US-09-215-221-56  
; Sequence 56, Application US/09215221  
; Patent No. 6265562  
; GENERAL INFORMATION:  
; APPLICANT: ELLERS, MARTIN  
; APPLICANT: RUEGIN, ANDREA  
; APPLICANT: SEDLACKER, HANS-HARALD  
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
; FILE REFERENCE: 026083/0192  
; CURRENT APPLICATION NUMBER: US/09/215,221  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 197 56 975.7  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 56  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Murine sp.  
; FEATURE:  
; OTHER INFORMATION: mutated p27  
;; US-09-215-221-56  
  
Query Match 98.2%; Score 377; DH 4; Length 135;  
Best Local Similarity 98.5%; Pred. No. 1.4e-41;  
Matches 60; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 DHRPSACNLFQGVNHHFLTRDLKRPDMEBASQPKWNPFGNKKPLEGKYVWQVFR 60  
DB 7 DHRPSACNLFQGVNHHFLTRDLKRPDMEBASQPKWNPFGNKKPLEGKYVWQVFR 66  
QY 61 GSLPEFY 67  
DB 67 GSLPEFY 73  
  
RESULT 8  
US-09-215-221-50  
; Sequence 50, Application US/09215221  
; Patent No. 6265562  
; GENERAL INFORMATION:  
; APPLICANT: ELLERS, MARTIN  
; APPLICANT: RUEGIN, ANDREA





US-09-215-221-55  
; Sequence 55, Application US/09215221  
; Patent No. 6265562  
; GENERAL INFORMATION:  
; APPLICANT: EILERS, MARTIN  
; APPLICANT: BUERGIN, ANDREA  
; APPLICANT: SEDLACKER, HANS-HARALD  
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
; FILE REFERENCE: 026083/0192  
; CURRENT APPLICATION NUMBER: US/09/215, 221  
; CURRENT FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 197 56 975, 7  
; PRIOR FILING DATE: 1997-12-20  
; NUMBER OF SEQ. ID NOS: 57  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 55  
; LENGTH: 180  
; TYPE: PRT  
; ORGANISM: Murine sp.  
; FEATURE:  
; OTHER INFORMATION: mutated p27  
US-09-215-221-55

Query Match 97.1%; Score 373; DB 4; Length 180;  
Best Local Similarity 97.0%; Pred. No. 6,6e-41;  
Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DHPKPSACRNLFGPVNHFFLTPDLFKHCPHMEFASQKKNPDPQNHKPIFGYFWQVEVER 60  
DB 7 DHPKPSACRNLFGPVNHFFLTPDLFKHCPHMEFASQKKNPDPQNHKPIFGYFWQVEVER 66  
OY 61 GSLPEFY 67  
DB 67 GSLPEFY 73

RESULT 13  
US-09-457-568-12  
; Sequence 12, Application US/09457568  
; Patent No. 6413943  
; GENERAL INFORMATION:  
; APPLICANT: McArthur, James G  
; APPLICANT: Gyuris, Jenio  
; APPLICANT: Finer, Mitchell H  
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of  
; TITLE OF INVENTION: Smooth Muscle Cells  
; FILE REFERENCE: 106482,691  
; CURRENT APPLICATION NUMBER: US/09/457, 568  
; CURRENT FILING DATE: 1999-12-09  
; EARLIER APPLICATION NUMBER: 60/122,974  
; EARLIER FILING DATE: 1999-03-01  
; EARLIER APPLICATION NUMBER: 60/163,682  
; EARLIER FILING DATE: 1999-11-05  
; NUMBER OF SEQ. ID NOS: 28  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-457-568-12

Query Match 96.1%; Score 369; DB 4; Length 177;  
Best Local Similarity 94.0%; Pred. No. 2,1e-40;  
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 DHPKPSACRNLFGPVNHFFLTPDLFKHCPHMEFASQKKNPDPQNHKPIFGYFWQVEVER 60  
DB 22 DHPKPSACRNLFGPVNHFFLTPDLFKHCPHMEFASQKKNPDPQNHKPIFGYFWQVEVER 81  
OY 61 GSLPEFY 67  
DB 82 GSLPEFY 88

RESULT 14  
US-09-457-646-12  
; Sequence 14, Application US/09457646  
; Patent No. 6420345  
; GENERAL INFORMATION:  
; APPLICANT: Patel, Sallil D  
; APPLICANT: McArthur, James G  
; APPLICANT: Gyuris, Jenio  
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of  
; TITLE OF INVENTION: Smooth Muscle Cells  
; FILE REFERENCE: 106482,287  
; CURRENT APPLICATION NUMBER: US/09/457, 646  
; CURRENT FILING DATE: 1999-12-09  
; EARLIER APPLICATION NUMBER: 60/122,974  
; EARLIER FILING DATE: 1999-03-01  
; EARLIER APPLICATION NUMBER: 60/163,682  
; EARLIER FILING DATE: 1999-11-05  
; NUMBER OF SEQ. ID NOS: 32  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-457-646-12

Query Match 96.1%; Score 369; DB 4; Length 177;  
Best Local Similarity 94.0%; Pred. No. 2,1e-40;  
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 DHPKPSACRNLFGPVNHFFLTPDLFKHCPHMEFASQKKNPDPQNHKPIFGYFWQVEVER 60  
DB 22 DHPKPSACRNLFGPVNHFFLTPDLFKHCPHMEFASQKKNPDPQNHKPIFGYFWQVEVER 81  
OY 61 GSLPEFY 67  
DB 82 GSLPEFY 88

RESULT 15  
US-09-215-221-51  
; Sequence 51, Application US/09215221  
; Patent No. 6265562  
; GENERAL INFORMATION:  
; APPLICANT: EILERS, MARTIN  
; APPLICANT: BUERGIN, ANDREA  
; APPLICANT: SEDLACKER, HANS-HARALD  
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
; FILE REFERENCE: 026083/0192  
; CURRENT APPLICATION NUMBER: US/09/215, 221  
; CURRENT FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 197 56 975, 7  
; PRIOR FILING DATE: 1997-12-20  
; NUMBER OF SEQ. ID NOS: 57  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 51  
; LENGTH: 194  
; TYPE: PRT  
; ORGANISM: Murine sp.  
; FEATURE:  
; OTHER INFORMATION: mutated p27  
US-09-215-221-51

Query Match 96.1%; Score 369; DB 4; Length 194;  
Best Local Similarity 95.5%; Pred. No. 2,4e-40;  
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 18 DHPKPSACRNLFGPVNHFFLTPDLFKHCPHMEFASQKKNPDPQNHKPIFGYFWQVEVER 77

QY 61 GALLERY 67  
111111  
11b 78 GALLERY 01

Search completed: May 8, 2003, 09:03:44  
Job Time: 6.02067 sec

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 04:58:32 ; Search time 6,8385 Seconds  
(without alignments)  
991.736 Million cell updates/sec

Title: US-09-865-018b-4\_COPY\_22\_88

Perfect score: 384  
Sequence: 1 DHPKPSACRNLPQVNHLEL PLEGRVFWQVPEPCSLPEFY 67

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 383519 seqs, 10123694 residues

Total number of hits satisfying chosen parameters. 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PublishedApplications\_AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
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- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	384	100.0	197	10	US-09-865-018-4
2	369	96.1	167	8	US-08-902-572-18
3	364	94.1	194	4	US-08-902-572-24
4	369	96.1	334	8	US-08-902-572-22
5	369	96.1	348	8	US-08-902-572-24
6	369	96.1	365	8	US-08-902-572-8
7	369	96.1	480	8	US-08-902-572-6
8	369	96.1	391	8	US-08-902-572-4
9	361	94.0	194	13	US-09-865-018-2
10	359	93.5	237	8	US-08-902-572-26
11	359	93.5	252	8	US-08-902-572-28
12	356	92.7	178	10	US-09-865-018-6
13	352	91.7	70	8	US-08-902-572-20
14	147	38.3	164	9	US-08-231-268-3
15	147	38.3	164	9	US-08-231-268-5
16	147	38.3	164	10	US-09-865-018-24
17	147	38.3	164	10	US-09-940-766-2
18	144	37.5	247	10	US-09-925-297-770
19	103	26.8	191	13	US-09-733-507-2

20	103	26.8	191	10	US-09-733-507-10
21	85	22.1	137	10	US-09-733-507-14
22	83.5	21.7	212	10	US-09-733-507-12
23	73	19.0	196	10	US-09-733-507-16
24	72	18.8	208	10	US-09-733-507-13
25	71.5	18.6	176	10	US-09-733-507-11
26	71	18.5	13	10	US-09-865-018-26
27	70	18.2	190	9	US-09-923-308-4
28	66	17.2	13	10	US-09-865-018-27
29	62.5	16.3	256	9	US-09-943-308-2
30	62	16.1	932	9	US-10-072-036-137
31	62	16.1	933	9	US-10-072-036-135
32	60	15.6	282	9	US-09-845-713A-2
33	60	15.6	552	9	US-09-819-142-22
34	59.5	15.5	398	9	US-10-001-254-14
35	59.5	15.5	536	9	US-09-866-050A-185
36	54.5	15.5	540	9	US-04-866-050A-409
37	54.5	15.5	786	9	US-10-164-080-2
38	54.5	15.5	787	9	US-09-866-050A-334
39	58.5	15.2	818	10	US-09-833-435A-11
40	57	14.8	317	9	US-09-925-299-853
41	57	14.8	317	10	US-09-925-299-853
42	57	14.8	474	10	US-09-529-063-40
43	56.5	14.7	313	1	US-08-781-986A-5197
44	56.5	14.7	806	12	US-10-003-405-2
45	56.5	14.7	1038	10	US-09-908-500A-2

## ALIGNMENTS

### RESULT 1

US-09-865-018-4

: Sequence 4, Application US/0985018

: Patent No US20020110886A1

: GENERAL INFORMATION:

: APPLICANT: Massague, Joan

: Robertis, James M.

: Koff, Andrew

: Polyak, Kornelia

: TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS

: PRODUCTION AND USE

: NUMBER OF SEQUENCES: 27

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: FOLEY, HOAG & ELIOT LLP

: STREET: One Post Office Square

: CITY: Boston

: STATE: MA

: COUNTRY: USA

: ZIP: 02109-2170

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/865,018

: FILING DATE: 24 May 2001

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US/08/854,039

: FILING DATE: 09 MAY 1997

: ATTORNEY/AGENT INFORMATION:

: NAME: Vincent, Matthew P.

: REGISTRATION NUMBER: 36,709

: REFERENCE/WORK NUMBER: MIV 079 04

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 617-832-1000

: TELEFAX: 617-832-7000

: INFORMATION FOR SEQ ID NO: 4:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 197 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

```

? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US 09 865 518 4

Query Match
Best Local Similarity 100.0% Score 984: 188 18: Length 197:
Patent No. US2002006870A1 Prod. No. 47a 47:
Matches 57: Conservative 0: Mismatches 0: Gaps 0:

QY DDPKSAVWELGAVWHELELEKLRKMLAQRKWNLDGKQKTLGKRWQVLR 60
|||||
DB 22 DDPKSAVWELGAVWHELELEKLRKMLAQRKWNLDGKQKTLGKRWQVLR 81

QY 6: GSLPEY 67
|||||
DB 82 GSLPEY 88

RESULT 2
US 08 902 572 18
? Sequence ID: Application US/0802572
? Patent No. US2002006870A1
? GENERAL INFORMATION:
? APPLICANT: Cygnus, Inc.
? APPLICANT: Lamphear, Don
? TITLE OF INVENTION: INHERITORS OF CELL CYCLE FREQUENCY AND
? TITLE OF INVENTION: RELATED THERETO
? NUMBER OF SEQUENCES: 44
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: POLLEY, BOB & ELLEN LLP
? STREET: One Post Office Square
? CITY: Boston
? STATE: MA
? COUNTRY: USA
? ZIP: 02109 2170
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: MS-DOS/MS-WIN
? SOFTWARE: Patent in Release #1.0, Version #1.40
? FILING DATE: 29 JUL 1997
? APPLICATION NUMBER: 08/092,572
? CLASSIFICATION: 614
? ATTORNEY/AGENT INFORMATION:
? NAME: Vincent, Matthew P.
? REGISTRATION NUMBER: 367,709
? REFERENCE/TRADE MARK NUMBER: MY 069,034
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617 842 7000
? TELEFAX: 617 842 7000
? INFORMATION FOR SEQ ID NO: 18:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 167 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? ORIENTATION: Linear
? MOLECULAR WEIGHT: protein
US 08 902 572 18

Query Match
Best Local Similarity 96.1% Score 369: 188 18: Length 167:
Patent No. US2002006870A1 Prod. No. 17a 46:
Matches 63: Conservative 0: Mismatches 0: Gaps 0:

QY DDPKSAVWELGAVWHELELEKLRKMLAQRKWNLDGKQKTLGKRWQVLR 60
|||||
DB 12 DDPKSAVWELGAVWHELELEKLRKMLAQRKWNLDGKQKTLGKRWQVLR 81

QY 6: GSLPEY 67
|||||
DB 72 GSLPEY 78

```

```

RESULT 3
US 09 970 561 2
? Sequence ID: Application US/990561
? Publication No. US2000024044A1
? GENERAL INFORMATION:
? APPLICANT: Nandabalan, Krishnan
? APPLICANT: Yano, Mutsaers
? TITLE OF INVENTION: p27(Kip 1) Family 12 Protein Complexes
? CLASSIFICATION: C12N 14/58N (1994) C12N 25/00
? CURRENT APPLICATION NUMBER: 09/799,970, 561
? PRIOR FILING DATE: 2001 10 04
? PRIOR APPLICATION NUMBER: 09/799,970-21,659
? PRIOR FILING DATE: 1999 06 18
? PRIOR APPLICATION NUMBER: 08/855,765
? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: Patent in Ver. 2.1
? SEQ ID NO 2
? LENGTH: 198
? TYPE: PRT
? ORGANISM: Homo sapiens
US 09 970 561 2

Query Match
Best Local Similarity 96.1% Score 669: 188 92: Length 198:
Matches 63: Conservative 4: Mismatches 0: Gaps 0:

QY 1 DDPKSAVWELGAVWHELELEKLRKMLAQRKWNLDGKQKTLGKRWQVLR 60
|||||
DB 22 DDPKSAVWELGAVWHELELEKLRKMLAQRKWNLDGKQKTLGKRWQVLR 81

QY 61 GSLPEY 67
|||||
DB 82 GSLPEY 88

RESULT 4
US 08 902 572 22
? Sequence ID: Application US/9802572
? Patent No. US2002006870A1
? GENERAL INFORMATION:
? APPLICANT: Cygnus, Inc.
? APPLICANT: Lamphear, Don
? APPLICANT: Beach, David H.
? TITLE OF INVENTION: INHERITORS OF CELL CYCLE FREQUENCY AND
? TITLE OF INVENTION: RELATED THERETO
? NUMBER OF SEQUENCES: 44
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: POLLEY, BOB & ELLEN LLP
? STREET: One Post Office Square
? CITY: Boston
? STATE: MA
? COUNTRY: USA
? ZIP: 02109 2170
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: MS-DOS/MS-WIN
? SOFTWARE: Patent in Release #1.0, Version #1.40
? FILING DATE: 29 JUL 1997
? APPLICATION NUMBER: 08/092,572
? CLASSIFICATION: 614
? ATTORNEY/AGENT INFORMATION:
? NAME: Vincent, Matthew P.
? REGISTRATION NUMBER: 367,709
? REFERENCE/TRADE MARK NUMBER: MY 069,034
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617 842 1000
? TELEFAX: 617 842 7000
? INFORMATION FOR SEQ ID NO: 22:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 404 amino acids

```

```

: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-09-902-572-22

Query Match          96.1%; Score 369; DB 8; Length 334;
Best Local Similarity 94.0%; Pred. No. 3.7e-35;
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACNLFPGVNHHELTLDLEKHCRCMEASQKKNWFDFQNHKPLEGKYWEVEK 60
:|||||
DB 22 EHPKPSACNLFPGVNHHELTLDLEKHCRCMEASQKKNWFDFQNHKPLEGKYWEVEK 81
:|||||

QY 61 GSLPEFY 67
:|||||
DB 82 GSLPEFY 88

RESULT 5
US-08-902-572-24
: Sequence 24, Application US/08902572
: Patent No. US20020068706A1
: GENERAL INFORMATION:
: APPLICANT: Gyuris, Jenö
: APPLICANT: Lamphere, Lou
: TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FOLEY, HOAG & ELIOT LLP
: STREET: One Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109-2170
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/902,572
: FILING DATE: 29-JUL-1997
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Vincent, Matthew P.
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MIV-069,03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-832-7000
: TELEFAX: 617-832-7000
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 348 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-902-572-24

Query Match          96.1%; Score 369; DB 8; Length 348;
Best Local Similarity 94.0%; Pred. No. 3.9e-35;
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACNLFPGVNHHELTLDLEKHCRCMEASQKKNWFDFQNHKPLEGKYWEVEK 60
:|||||
DB 22 EHPKPSACNLFPGVNHHELTLDLEKHCRCMEASQKKNWFDFQNHKPLEGKYWEVEK 81
:|||||

QY 61 GSLPEFY 67
:|||||
DB 82 GSLPEFY 88
```

```

RESULT 6
US-08-902-572-8
: Sequence 8, Application US/08902572
: Patent No. US20020068706A1
: GENERAL INFORMATION:
: APPLICANT: Gyuris, Jenö
: APPLICANT: Lamphere, Lou
: TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FOLEY, HOAG & ELIOT LLP
: STREET: One Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109-2170
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/902,572
: FILING DATE: 29-JUL-1997
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Vincent, Matthew P.
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MIV-069,03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-832-7000
: TELEFAX: 617-832-7000
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 365 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-902-572-8

Query Match          96.1%; Score 363; DB 8; Length 365;
Best Local Similarity 94.0%; Pred. No. 4.1e-35;
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACNLFPGVNHHELTLDLEKHCRCMEASQKKNWFDFQNHKPLEGKYWEVEK 60
:|||||
DB 18 EHPKPSACNLFPGVNHHELTLDLEKHCRCMEASQKKNWFDFQNHKPLEGKYWEVEK 248
:|||||

QY 61 GSLPEFY 67
:|||||
DB 249 GSLPEFY 255

RESULT 7
US-08-902-572-6
: Sequence 6, Application US/08902572
: Patent No. US20020068706A1
: GENERAL INFORMATION:
: APPLICANT: Gyuris, Jenö
: APPLICANT: Lamphere, Lou
: TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FOLEY, HOAG & ELIOT LLP
: STREET: One Post Office Square
: CITY: Boston
: STATE: MA
```



Db 22 DHPKPSACNLPGFVNHEELTDLEKHCKDMEASQKWNFDQNHKPLEGKYEWQEVER 81

QY 61 GSLPEFY 67  
| | | | |  
Db 82 GSLPEFY 88

RESULT 10  
US-08-902-572-26  
; Sequence 26, Application US/08092572  
; Patent No. US20020068706A1  
; GENERAL INFORMATION:  
; APPLICANT: Gyuris, Jenö  
; APPLICANT: Lampert, Lou  
; APPLICANT: Beach, David H.  
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND  
; TITLE OF INVENTION: RELATED THERETO  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,572  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MIV-069 03  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 237 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-902-572-26

Query Match 93.5%; Score 359; DB 8; Length 237;  
Best Local Similarity 92.5%; Pred No. 3, 7e-34;  
Matches 62; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPKPSACNLPGFVNHEELTDLEKHCKDMEASQKWNFDQNHKPLEGKYEWQEVER 60  
| | | | |  
Db 9 DYAKPSACNLPGFVNHEELTDLEKHCKDMEASQKWNFDQNHKPLEGKYEWQEVER 68  
QY 61 GSLPEFY 67  
| | | | |  
Db 69 GSLPEFY 75

RESULT 11  
US-08-902-572-26  
; Sequence 28, Application US/08092572  
; Patent No. US20020068706A1  
; GENERAL INFORMATION:  
; APPLICANT: Gyuris, Jenö  
; APPLICANT: Lampert, Lou  
; APPLICANT: Beach, David H.  
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND  
; TITLE OF INVENTION: RELATED THERETO

QY 1 DHPKPSACNLPGFVNHEELTDLEKHCKDMEASQKWNFDQNHKPLEGKYEWQEVER 60  
| | | | |  
Db 9 DYAKPSACNLPGFVNHEELTDLEKHCKDMEASQKWNFDQNHKPLEGKYEWQEVER 68  
QY 61 GSLPEFY 67  
| | | | |  
Db 69 GSLPEFY 75

RESULT 12  
US-09-865-018-6  
; Sequence 6, Application US/09865018  
; Patent No. US20020110886A1  
; GENERAL INFORMATION:  
; APPLICANT: Massague, Joan  
; APPLICANT: Roberts, James M.  
; APPLICANT: Koff, Andrew  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS  
; PRODUCTION AND USE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/865,918  
; FILING DATE: 24-May-2001

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:  
; ADDRESS: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/902,572  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MIV-069 03  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-902-572 28

Query Match 93.5%; Score 359; DB 8; Length 252;  
Best Local Similarity 92.5%; Pred No. 3, 9e-34;  
Matches 62; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPKPSACNLPGFVNHEELTDLEKHCKDMEASQKWNFDQNHKPLEGKYEWQEVER 60  
| | | | |  
Db 9 DYAKPSACNLPGFVNHEELTDLEKHCKDMEASQKWNFDQNHKPLEGKYEWQEVER 68  
QY 61 GSLPEFY 67  
| | | | |  
Db 69 GSLPEFY 75

RESULT 12  
US-09-865-018-6  
; Sequence 6, Application US/09865018  
; Patent No. US20020110886A1  
; GENERAL INFORMATION:  
; APPLICANT: Massague, Joan  
; APPLICANT: Roberts, James M.  
; APPLICANT: Koff, Andrew  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS  
; PRODUCTION AND USE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/865,918  
; FILING DATE: 24-May-2001





Query Match 38.3%, Score 147, DB 9, length 164;  
 Best Local Similarity 42.68%, Pred. No. 1, le-09;  
 Matches 26; Conservative 11; Mismatches 24; Indels 3, Gaps 0;

QY 7 ACNIEGPNVNHFFITNDLEKHCORMEFAAQKKNWDFCONHKPIETGYEWQVDFVPGSLPEF 66  
 ||| ||||| : ||| : : ||||| |||| : | : |||  
 Db 17 ACKRIFGPVDSFQISDPDTALMAGSTQCAPPEWNEFVETPTLEQDFAMERVPGIGLPKI 76  
 QY 67 Y 67  
 Db 77 Y 77

Search completed: May 30, 2003, 09:05:11  
 Job time : 7.845 secs



GenCafe version 5.1.6  
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OM protein protein search, using sw model

Run on: May 30, 2003, 08:54:42 : Search time 5.62662 seconds  
(without alignments)  
1144.739 Million cell updates/sec

Title: US-09-865-018b-4\_COPY\_22\_88

Perfect score: 384

Sequence: 1 DHPKPSACRNLFQGVNHEEL..... PLEGRYWQFVERGSIPEFY 67

Scoring table: BLOSUM62

Gapop 10 0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is defined by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	384	100.0	197	2 149064	cyclin-cdk inhibit
2	373	97.1	194	2 152718	gene p27Kip1 prote
3	179	46.6	316	2 G02424	cyclin-dependent k
4	173	45.1	210	2 151683	cyclin-dependent k
5	171	44.5	348	2 149262	cyclin cdk inhibit
6	154	40.1	164	2 184726	tumor suppressor p
7	147	38.3	181	2 186674	cyclin-dependent k
8	145	37.8	181	2 154380	cyclin-dependent k
9	140	36.5	154	2 149023	tumor suppressor p
10	137	35.7	143	2 A49438	p53 tumor suppress
11	115.5	33.1	258	2 T24499	hypothetical prote
12	103	26.8	191	2 T01132	cyclin-dependent k
13	87.5	22.8	184	2 T24406	hypothetical prote
14	73	19.0	146	2 T04404	hypothetical prote
15	72	18.8	195	2 H96542	hypothetical prote
16	71.5	18.6	209	2 T46140	hypothetical prote
17	69	18.0	327	2 T06707	hypothetical prote
18	69	18.0	470	2 S50083	phthalase - short
19	65.5	17.1	246	1 S49770	hypothetical prote
20	65.5	17.1	489	2 S83401	hypothetical prote
21	65	16.9	611	1 S12566	translation initia
22	61.5	16.5	407	2 T20804	hypothetical prote
23	63	16.4	348	2 T52126	mitogen-activated
24	63	16.4	348	2 T51340	mitogen-activated
25	63	16.4	413	2 A59356	hypothetical prote
26	62	16.4	533	2 S20346	deoxyribodipyrimid
27	62.5	16.3	725	1 T18P02	gene 1 protein - p
28	62.5	16.3	496	2 T18P02	100 kDa activator
29	62.5	16.3	955	2 S64449	centromere-binding

#### ALIGNMENTS

##### RESULT 1

I49064

cyclin-cdk inhibitor p27 - mouse

N:Alternate names: Cbl p27; G1 cyclin-cyclin-dependent kinase inhibitor p27

C:Species: Mus musculus (house mouse)

C>Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 05-Nov-1999

C:Accession: I49064

R:Toyoshima, H.; Hunter, T.

Cell 78, 67-74, 1994

A:Title: p27, a novel inhibitor of G1 cyclin Cdk protein kinase activity, is related

A:Reference number: A54819; MIM:143365; PMID:8033213

A:Accession: I49064

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197-RES-

A:Cross-references: EMBL:U010440; NID:553277; PIR:AAA21149.1; FID:9532772

C:Keywords: cell cycle; control

Query Match 100.0%; Score 384; DB 2; Length 197;

Best Local Similarity 100.0%; Pred No 1 3e-16;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACRNLFQGVNHEELTDLKHKCKMEASQKWNFDQNHKPLEGRYWEVER 60

DB 22 DHPKPSACRNLFQGVNHEELTDLKHKCKMEASQKWNFDQNHKPLEGRYWEVER 81

QY 61 GSLPEFY 67

DB 82 GSLPEFY 88

##### RESULT 2

I52718

gene p27Kip1 protein - human

C:Species: Homo sapiens (man)

C>Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000

C:Accession: I52718

R:Pietenpol, J.A.; Richlander, S.K.; Sato, Y.; Papadopoulos, N.; Liu, B.; Friedman, C.

Cancer Res. 55, 1206-1210, 1995

A:Title: Assignment of the human p27Kip1 gene to 12p13 and its analysis in leukemias.

A:Reference number: I52718; MIM:15528144; PMID:7882309

A:Accession: I52718

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-198-RES-

A:Cross-references: GB:S4088; NID:9408402; FID:AA014244.1; FID:34261944

C:Genetics:

A:Gene: p27Kip1

A:Introns: 159/1

Query Match 97.1%; Score 373; DB 2; Length 198;

Best Local Similarity 95.5%; Pred. No. 2.4e-35;



```

QY      7 ACNNI PCPVNHEFLTDLEKHCORMPFASQRKNWDFQNHHKPIECGYFYWEQVEFGSLPEEF 63
       ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     34 ACPPLPCPVNSEQLPFIWTALMAAGTICAPFPWNFCVFTETPIELIPAFMERVGILGLPKL 93

QY      57 Y 57
       |
Db     94 Y 94

RESULT 9
149023
tumor suppressor p21 WAF1/Cip1 [imported] - mouse
C:Species: Mus musculus (house mouse)
C:date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20 Jun-2000
C:Accession 149023; I49296
R:Harupp, K., Siwarski, D., Dosik, J., Michieli, P., Chetid, M.; Reed, S.; Moock
Oncogene 9, 3017-3020, 1994
A:title: Molecular cloning, sequencing, chromosomal localization and expression
A:Reference number 149023; MIDB:94366751; PMID 8084507
A:Accession: 149023
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1159 -RES>
A:Cross-references EMBL:U09507; NID:3545302; PIDN:AAR60456_1; PID:g595303
E:EJL-BIRY, WS.; Takiguchi, T.; Walchman, T.; Velculescu, V.; Linzer, L.D.; Burren
Cancer Res. 55, 2910-2919, 1995
A:title: Topological control of p21WAF1/Cip1 expression in normal and neoplas
A:Reference number: 149296; MCID:95316868; PMID:7796420
A:Accession: 149296
A>Status: nucleic acid sequence not shown, translation not shown, translated
A:Molecule type: mRNA
A:Residues: 1159 -FEQ>
A:Cross-references EMBL:U14174; NID:302678; PIN:AA6226_1; PID:g02679
C:Genetics:
A:Gene: Waf1

```

[illegible]

A49438  
p53 tumor suppression mediator WAF1 - mouse (fragment)  
C.Species: Mus musculus (house mouse)  
C.Date: 07-Apr-1994 #s-synonym\_revision: 18-Nov-1994  
C.Accession: A49438  
C.Publication: Watanabe, T., Yokoyama, Y. E., 1993, B.R.J. Pursons, P., Trent  
Cell 75, 817-825, 1993  
A.Title: WAF1, a putential mediator of p53 tumor suppression.  
A.Reference number: A49438; PMID:94061997; PMID:824752  
A.Accession: A49438  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-143 <ELL>  
A.Note: sequence extracted from NCBI backbone (NCBIN:140807, NCBIPI:140808)

QY 4 KPZAFNLFPGVNVHEELITOLEKHKFCOMEASDCKWNFUPYNHKPLFGPYEWEVERGSL 63  
+ + + + + . . . . . : : : : : + + + + +  
+ + + + +

QB KSKVLPGLFPGVISEULSPDCLAMAGLCPFAFPWFNFDFVIIFOLGNFVWFKVRKSJCL 72  
+ + + + + . . . . . : : : : : + + + + +









GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 09:52:42 : Search time 2 sec 59 seconds  
(without alignments)  
972,808 Million cell updates/sec

Title: us-09-865-018b-4\_copy\_22\_88

Perfect score: 384

Sequence: 1 DRPRPSAERNNRFGVNHEFL

PIEKRYHWVERGSLPEFY 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	384	100.0	197	1	CDNB_MOUSE
2	369	96.1	198	1	CDNB_HUMAN
3	368	95.8	198	1	CDNB_FELCA
4	366	95.3	198	1	CDNB_CRIGR
5	356	92.7	178	1	CDNB_MUSVI
6	174	46.6	316	1	CDNC_HUMAN
7	171	44.5	348	1	CDNC_MOUSE
8	147	38.3	164	1	CDN1_HUMAN
9	143	37.2	164	1	CDN1_FELCA
10	140	36.5	159	1	CDN1_MOUSE
11	68	17.7	532	1	RHP_FOTFE
12	65.5	17.1	489	1	YN98_YEAST
13	65	16.9	611	1	IF4B_HUMAN
14	62.5	16.3	724	1	V501_HRP22
15	62.5	16.3	956	1	CR31_YEAST
16	62	16.1	670	1	K2FA_BOVIN
17	62	16.1	670	1	K2FA_HUMAN
18	62	16.1	670	1	K2FA_FARIT
19	62	16.1	686	1	KGPB_BOVIN
20	62	16.1	686	1	KGPB_HUMAN
21	62	16.1	686	1	KGPR_MOUSE
22	61.5	16.0	804	1	RNF5_YEAST
23	61	15.9	450	1	INVO_LERCA
24	60	15.6	382	1	PMT_HUMAN
25	59.5	15.5	398	1	DAP3_HUMAN
26	59	15.4	261	1	YC52_RABIN
27	59	15.4	417	1	YAC1_YEAST
28	59	15.4	523	1	33HL_LYCES
29	59	15.4	805	1	SUS1_SOLITU
30	59	15.4	805	1	SUS1_LYCES
31	59	15.4	808	1	SUS1_DAUCA
32	59	15.4	2717	1	2ET1_HUMAN
33	58.5	15.2	171	1	Y501_CAPPL

RESULT 1

ID	CDNB_MOUSE	STANDARD	PRT	197 AA
AC	P46414			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15 JUN 2002 (Rel. 41, Last annotation update)			
DE	Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase inhibitor p27) (p27Kip1).			
GN	CDKN1B			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;			
UX	NCBI_TaxID=10090;			
RN	[1]			
RX	MEDLINE=94306519; PubMed=8033213;			
RA	Toyoshima H., Hunter T.;			
RT	"p27, a novel inhibitor of G1 cyclin-cdk protein kinase activity, is related to p21."			
RL	Cell 78:67-74(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
PC	TISSUE=Embryo;			
PX	MEDLINE=94306519; PubMed=8033213;			
RA	Polyak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M., Tempst P., Massague J.;			
RT	"Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a potential mediator of extracellular antimitogenic signals."			
RL	Cell 78:59-66(1994).			
RN	[3]			
RP	INTERACTION WITH NUP50, AND MUTAGENESIS.			
PC	STRAIN=BALB/c;			
PX	MEDLINE 2021857; PubMed=13811698;			
RA	Mueller D., Thieke K., Buerger A., Dickmanns A., Eilers M.;			
RT	"Cyclin E-mediated elimination of p27 requires its interaction with the nuclear pore-associated protein NUP50."			
PL	EMBO J. 19:3168-3180(2000).			
CC	... FUNCTION: Involved in G1 arrest. May mediate 14k beta-induced G1 arrest. Binds to and inhibits complexes formed by cyclin E-CDK2, cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin NUP50 is required for nuclear import and for degradation of phosphorylated p27Kip1 after nuclear import.			
CC	-1- SUBUNIT: Interacts with NUP50.			
CC	-1- SUBCELLULAR LOCATION: Nuclear.			
CC	-1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.			
CC	-----			
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CC	-----			
CC	EMBL: U10440; AAA21149.1; -			

023736 brassica ju  
P40797 drosophila  
F11325 saccharomyc  
Q94711 schizosarc  
P12093 oryza sativ  
P34431 caenorhabdi  
P76045 escherichia  
P96749 corynebacte  
P33294 kluyveromyc  
Q24702 drosophila  
P56786 arabidopsis  
Q97577 homo sapien



CC - FUNCTION: Involved in G1 arrest. May mediate TGF-beta induced G1  
CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,  
CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin  
CC NUP50 is required for nuclear import and for degradation of  
CC phosphorylated p27Kip1 after nuclear import (By similarity).  
CC - SUBUNIT: Interacts with NUP50 (By similarity).  
CC - SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC - SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.  
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CC  
CC EMBL: U84649; BAA23167.1; .  
CC InterPro: IPR003175; CDI: 1.  
CC Pfam: PF02234; CDI: 1.  
CC Cell cycle: Nuclear protein.  
CC FT DOMAIN: 153..165 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
CC SEQUENCE 198 AA: 22249 MW: 54552P2146293854 CRC64;  
CC  
CC Query Match 95.8%; Score 368; DB 1; Length 198;  
CC Best local Similarity 94.0%; Pred. No. 2.3e-34;  
CC Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 DHKPSACNLPFGVNVHEELTFLKHKCRDMEASQKWNFDQNHKPLEGYEWQVEVER 60  
CC :|||||  
CC Db 22 EHPKPSACNLPFGVNVHEELTFLKHKCRDMEASQKWNFDQNHKPLEGYEWQVEVER 81  
CC  
CC QY 61 GSLPEFY 67  
CC :|||||  
CC Db 82 GSLPEFY 88  
CC  
CC Query Match 95.8%; Score 368; DB 1; Length 198;  
CC Best local Similarity 94.0%; Pred. No. 2.3e-34;  
CC Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 DHKPSACNLPFGVNVHEELTFLKHKCRDMEASQKWNFDQNHKPLEGYEWQVEVER 60  
CC :|||||  
CC Db 22 EHPKPSACNLPFGVNVHEELTFLKHKCRDMEASQKWNFDQNHKPLEGYEWQVEVER 81  
CC  
CC QY 61 GSLPEFY 67  
CC :|||||  
CC Db 82 GSLPEFY 88  
CC  
CC RESULT 4  
CC CONBL\_CRIGR STANDARD: PRT: 198 AA.  
CC AC Q60439;  
CC DT 01-NOV-1997 (Rel. 35, Created)  
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
CC DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase  
CC inhibitor p27) (p27Kip1) (p30 Kip1).  
CC GN CDKN1B OR KIP1.  
CC OS Cricetus griseus (Chinese hamster).  
CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
CC Cricetulus.  
CC OX NCBI\_TaxID=10029;  
CC RN [1]  
CC RP SEQUENCE FROM N.A.  
CC RC TISSUE=Lung;  
CC RX MEDLINE=97471701; PubMed 930642;  
CC RA Parekh H B, Pilliarisetty K, Kozupoli S, Simpkins H J  
CC RT Isolation of a hamster cDNA homologous to the mouse and human cyclin  
CC RT kinase inhibitory protein p27Kip1.  
CC RC Somai, Cell Mol. Genet. 23:147-151(1997).  
CC - FUNCTION: Involved in G1 arrest. May mediate TGF-beta-induced G1  
CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,  
CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin  
CC NUP50 is required for nuclear import and for degradation of  
CC phosphorylated p27Kip1 after nuclear import (By similarity).  
CC - SUBUNIT: Interacts with NUP50 (By similarity).  
CC - SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC - SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.  
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CC  
CC EMBL: U84649; BAA23167.1; .  
CC InterPro: IPR003175; CDI: 1.  
CC Pfam: PF02234; CDI: 1.  
CC Cell cycle: Nuclear protein.  
CC FT DOMAIN: 153..165 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
CC SEQUENCE 198 AA: 22249 MW: 54552P2146293854 CRC64;  
CC  
CC Query Match 95.3%; Score 366; DB 1; Length 198;  
CC Best local Similarity 92.5%; Pred. No. 3.9e-34;  
CC Matches 62; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
CC  
CC QY 1 DHKPSACNLPFGVNVHEELTFLKHKCRDMEASQKWNFDQNHKPLEGYEWQVEVER 60  
CC :|||||  
CC Db 22 EHPKPSACNLPFGVNVHEELTFLKHKCRDMEASQKWNFDQNHKPLEGYEWQVEVER 81  
CC  
CC QY 61 GSLPEFY 67  
CC :|||||  
CC Db 82 GSLPEFY 88  
CC  
CC RESULT 5  
CC CONBL\_MUSVI STANDARD: PRT: 178 AA  
CC AC P46529;  
CC DT 01-NOV-1995 (Rel. 42, Created)  
CC DT 01-NOV-1995 (Rel. 42, Last sequence update)  
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
CC DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase  
CC inhibitor p27) (p27Kip1) (Fragment).  
CC GN CDKN1B.  
CC OS Mus musculus (American mink).  
CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
CC Mustela.  
CC OX NCBI\_TaxID=9667;  
CC RN [1]  
CC RP SEQUENCE FROM N.A.  
CC RC TISSUE=Lung;  
CC RX MEDLINE=94306518; PubMed-8033212;  
CC RA Polyak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M.,  
CC Tempst P., Massague J.;  
CC RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a  
CC potential mediator of extracellular antimitogenic signals.";  
CC Cell 78:59-66(1994).  
CC GN [2]  
CC RP FUNCTION.  
CC RX MEDLINE=94115862; PubMed=8288131;  
CC RA Polyak K., Kato T.-Y., Solomon M J, Sherr C.J., Massague J.,  
CC Roberts J.M., Koff A.;  
CC RT "p27Kip1, a cyclin-Cdk inhibitor, links transforming growth  
CC factor-beta and contact inhibition to cell cycle arrest.";  
CC Genes Dev. 8:9-22(1994).  
CC - FUNCTION: Involved in G1 arrest. May mediate TGF-beta-induced G1  
CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,  
CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin  
CC NUP50 is required for nuclear import and for degradation of  
CC phosphorylated p27Kip1 after nuclear import (By similarity).  
CC - SUBUNIT: Interacts with NUP50 (By similarity).  
CC - SUBCELLULAR LOCATION: Nuclear.  
CC - SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.  
CC  
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CC







```

RL Cell 75:817-825(1993).
CC -!- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
CC ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
CC DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
CC ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
CC KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- INDUCTION: BY P53, MEZEREIN (ANTILEUKEMIC COMPOUND) AND INTERFERON
CC BETA.
CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
CC
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CC
CC EMBL: D26020; BAA05041.1; -.
CC InterPro: IPR000474; DNA_photolyase.
CC InterPro: IPR000288; DNA_photolyase_2.
CC InterPro: IPR005101; FAD_binding_7.
CC Pfam: PF00875; DNA_photolyase; 1.
CC Pfam: PF03441; FAD_binding_7; 1.
CC ProDom: PD007711; DNA_photolyase_2; 1.
CC PROSITE: PS01083; DNA_PHOTOLYASES_2; 1.
CC PROSITE: PS01084; DNA_PHOTOLYASES_2; 1.
CC Lyase, Chromophore; Flavoprotein, FAD, DNA repair, DNA-binding.
CC
CC QUERY MATCH 17.7% Score 68, DB 1; Length 532,
CC Best Local Similarity 29.3%; Pred. No. 3.2;
CC Matches 22, Conservative 13, Mismatches 22, Indels 18, Gaps 4;
CC
QY 1 DHKPSACRNLU-----PGVNHHEELTRDLEKH-----CRDMEASORKW---NFDF- 43
Db 323 NN--NKALSNLSWFFHFGVSVQVPAILEVJKHKSVMYLSVTNVEEAVVPELADNCFY 382
QY 44 -ONHKPLEGRIEWOE 57
Db 383 NKNYDKLEGAYDWAQ 397

RESULT 12
YN98_YEAST
ID YN98_YEAST STANDARD; PRT: 489 AA.
AC P53755;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 54.8 kDa protein in B103-HXT17 intergenic region.
GN YNR069C OR N3555.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
FP SEQUENCE FROM N A
FA Dusterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
FA Hilbert H., Moestl D.;
FA Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO THE N-TERMINAL OF YEAST BULL AND YML11W.
CC
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CC
CC EMBL: Z71684; CAA96351.1; -.
CC SCD; S0005352; YNR069C.
CC KW Hypothetical protein.
CC
CC QUERY MATCH 17.1% Score 65.5; DB 1; Length 489;
CC Best Local Similarity 24.1%; Pred. No. 5.6;
CC Matches 19; Conservative 10; Mismatches 15; Indels 35; Gaps 3;
CC
QY 14 PVNHEELTRDLEK-----HCRDMEASORKWNDFONHNP 48

```

[illegible]



```

RESULT 15
CB31_YEAST
ID CB31_YEAST STANDARD; PRT: 956 AA.
AC P32504;
DT 01-OCT-1993 (rel. 27, Created)
DT 01-OCT-1993 (rel. 27, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Centromere DNA binding protein complex CBF3 subunit A (Kinetochores
DE protein CTF14) (Centromere-binding factor 2).
GN CBF3 OR CBF3A OR NDC10 OR CTF14 OR CBF2 OR YGR140W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID:4932;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP MEDLINE=93252988; PubMed=8486733;
RA Jiang W., Lechner J., Carbon J.;
RT "Isolation and characterization of a gene (CBF2) specifying a protein
RT component of the budding yeast kinetochore."
RL J. Cell Biol. 121:513-519(1993).
RN [2]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP MEDLINE=93252987; PubMed=8486732;
RA Goh P.-Y., Kilmartin J.V.;
RT "NDC10: a gene involved in chromosome segregation in Saccharomyces
RT cerevisiae."
RL J. Cell Biol. 121:503-512(1993).
RN [3]
RN SEQUENCE FROM N.A.
RP van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talla E.,
RA Nawrocki A., del Bino S., Goffeau A.;
EL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: ESSENTIAL FOR CHROMOSOME SEGREGATION AND MOVEMENT OF
CC CENTROMERES ALONG MICROTUBULES. IT PLAYS A ROLE IN THE ATTACHMENT
CC OF CHROMOSOMES TO THE SPINDLE. CBF3 BINDS SELECTIVELY TO A HIGHLY
CC CONSERVED DNA SEQUENCE CALLED CDEIII, FOUND IN CENTROMERES AND IN
CC SEVERAL PROMOTERS.
CC -!- SUBUNIT: CBF3 IS FORMED OF FOUR SUBUNITS, CBF3A (CBF2), CBF3B
CC (CBF3), CBF3C (CTF13) AND CBF3D. STRONGLY INTERACTS WITH BIR1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
DR EMBL: Z21627; CAA79753.1; -
DR EMBL: X69300; CAA49158.1; -
DR EMBL: Z72925; CAA97153.1; -
DR PIR: A46432; A46432.
DR PIR: A46433; A46433.
DR SGD: S0003372; CBF2.
DR KW Nuclear protein; Chromosomal protein; DNA-binding; Centromere.
DR FT CONFLICT 774 774 K -> Q (IN REF. 1).
SQ SEQUENCE 956 AA; 111917 MW; C93FB/E033931E3D CRC64;
Query Match 16.3%, Score 62.5; DB 1, Length 956;
Best Local similarity 40.5%; Pred. No. 26;
Matches 17; Conservative 2; Mismatches 12; Indels 11, Gaps 2;
QY 15 VNHEELTR---DLEKHCQDEEAS-----QKKWNDFQN 45
DB 904 VNHELDYKAVTIPKTIQNEGFSFSLAKPLRKWRHDQN 945

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Search completed: May 30, 2003, 08:59:10  
Job time : 3.85659 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 06:55:57 : Search time 11:56:30 seconds  
(without alignments)  
1181.337 Million cell updates/sec

Title: US-09-865-018b-4\_copy\_22\_88

Perfect score: 384

Sequence: 1 FAPKPSA<P>NLFQVNHDEL

Scoring table: PROSUM62

Gapop 10.0, Gapext 0.5

Searched: 671586 seqs, 266047115 residues

Total number of hits satisfying chosen parameters: 671583

Minimum DB seq length: 0

Maximum DB seq length: 266000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_muc:\*
- 8: sp\_orquaele:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_protist:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacterioph:\*
- 17: sp\_archaeap:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	380	99.0	197	11	008769	008769 rattus norv
2	380	99.0	197	11	035792	035792 rattus norv
3	373	97.1	198	4	Q96TE0	Q96TE0 homo sapien
4	369	96.1	198	4	043806	043806 homo sapien
5	369	96.1	198	4	Q9NY36	Q9NY36 homo sapien
6	369	96.1	198	4	Q9HUS6	Q9HUS6 homo sapien
7	368	95.8	172	6	Q9HEA5	Q9HEA5 sus scrofa
8	368	95.8	198	6	Q9HDC3	Q9HDC3 sus scrofa
9	227.5	59.2	179	13	Q90YX4	Q90YX4 brachydontic
10	173	45.1	210	13	Q91603	Q91603 xenopus lae
11	171	44.5	335	11	Q91V06	Q91V06 mus musculus
12	169	44.0	209	13	Q91646	Q91646 xenopus lae
13	154	40.1	164	11	Q64315	Q64315 rattus norv
14	147	38.3	164	4	Q96LE1	Q96LE1 homo sapien
15	145	37.8	181	4	Q1401C	Q1401C homo sapien
16	115.5	30.1	258	5	Q22198	Q22198 caenorhabdi

17	109	28.1	259	5	Q96P65	Q96P65 caenorhabdi
18	103	26.8	191	10	Q04154	Q04154 arabidopsis
19	103	26.8	191	10	Q96P65	Q96P65 arabidopsis
20	89.6	23.3	253	5	Q96P65	Q96P65 arabidopsis
21	88	22.9	164	10	Q94V92	Q94V92 nicotiana t
22	87.5	22.8	184	5	Q22197	Q22197 caenorhabdi
23	85	22.1	222	10	Q9FK95	Q9FK95 arabidopsis
24	84.5	21.7	192	10	Q9FS28	Q9FS28 fusum sativ
25	83.5	21.7	196	10	Q9LJL5	Q9LJL5 arabidopsis
26	82	21.4	159	10	Q93YF6	Q93YF6 nicotiana s
27	82	21.4	245	5	Q94536	Q94536 drosophila
28	82	21.4	255	5	Q91654	Q91654 drosophila
29	80	20.8	245	5	Q91654	Q91654 drosophila
30	80	20.8	246	10	Q94X60	Q94X60 arabidopsis
31	80	20.8	289	10	Q94X60	Q94X60 arabidopsis
32	78	20.3	189	10	Q95RY0	Q95RY0 arabidopsis
33	73	19.0	196	10	Q94597	Q94597 chenopodium
34	72	18.8	195	10	Q9FX90	Q9FX90 arabidopsis
35	72	18.8	195	10	Q94CL9	Q94CL9 arabidopsis
36	71.5	18.6	209	10	Q9SCR2	Q9SCR2 arabidopsis
37	71	18.5	105	5	Q77670	Q77670 canis fami
38	70	18.2	242	10	Q9FW65	Q9FW65 oryza sativ
39	70	18.2	647	5	Q9VC60	Q9VC60 drosophila
40	69	18.0	249	16	Q9XN35	Q9XN35 clostridium
41	69	18.0	470	6	Q28464	Q28464 monodelphis
42	67	17.4	532	5	Q61133	Q61133 dictyosteli
43	65.5	17.1	204	15	Q9YU29	Q9YU29 human immun
44	65.5	17.1	246	3	Q03973	Q03973 saccharomyc
45	64.5	16.8	509	2	Q93F40	Q93F40 shigella fl

#### ALIGNMENTS

RESULT 1

008769 PRELIMINARY: PRT: 197 AA.

AC 008769;  
DT 01-JUL-1997 (TREMREL. 04, Created)  
DT 01-JUL-1997 (TREMREL. 04, Last sequence update)  
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
DE P27 KIPL.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kawada M., Yamagoe S., Uehara Y.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kawada M., Yamagoe S., Karuo S., Mizuno S., Uehara Y.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Kawada M., Yamagoe S., Murakami Y., Suzuki K., Mizuno S., Uehara Y.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY;  
PA Easton F., Feist M.A.;  
PL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases  
DR FMR1, F6924, BAA19968.1, ...  
PF EMBL: AF015194; AAB71368.1; ...  
DE In-ep3, IF003175, CDI.  
DE Ffam, FF02234, CDI, 1  
SQ SEQUENCE 197 AA; 22139 MW: 55738078C209847F CRC64;

Query Match 99.0%; Score 380; DB 11; Length 197;  
Best local Similarity 98.5%; Pred. No. 6.4e-35;  
Matches 66; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DHPKSAACRRLTCTVQVHRLTLEKLEKPEKMEASQKKNKFFQNIKPLKRYVQVVER 60
DB 22 DHPKSAACRRLTCTVQVHRLTLEKLEKPEKMEASQKKNKFFQNIKPLKRYVQVVER 60
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 2
QY 045792 PRELIMINARY: PFI: 197 AA.
AC 045792:
DI 01 JAN 1998 (TEMBLrel, 05, Created)
DI 01 JAN 1998 (TEMBLrel, 19, Last sequence update)
DI 01 DEC 2001 (TEMBLrel, 19, Last annotation update)
DE p27.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Lox10-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN: GK2567, Tissue: Spleen.
RX MEDLINE 97461761; PubMed 9218722;
KA Nomura H., Sakada Y., Fujinaga K., Ohtaki S.;
ET Molecular and characterisation of rat p27Kip1, a cyclin-dependent
RT Kinase inhibitor";
RL Gene 191:211-218(1997);
DR EMBL: D83792; BAA21561.1;
DR InterPro: IPR003175; CDI: 1;
DR Pfam: PF02244; CDI: 1;
SQ SEQUENCE 197 AA, 22112 MW, 557807852055462 CRC64;

Query Match 99.08; Score 380; DB 11; Length 197;
Best Local Similarity 98.58; Pred. No. 6.4e 45;
Matches 66; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKSAACRRLTCTVQVHRLTLEKLEKPEKMEASQKKNKFFQNIKPLKRYVQVVER 60
DB 22 DHPKSAACRRLTCTVQVHRLTLEKLEKPEKMEASQKKNKFFQNIKPLKRYVQVVER 60
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 3
QY 045792 PRELIMINARY: PFI: 198 AA.
AC 045792:
DI 01 DEC 2001 (TEMBLrel, 19, Created)
DI 01 DEC 2001 (TEMBLrel, 19, Last sequence update)
DI 01 MAR 2002 (TEMBLrel, 20, Last annotation update)
DE CDK inhibitor p27KIP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Lox10-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE 20472729, PubMed 10941178;
KA McIlard S.S., Vidal A., Markus M., Kott A.;
ET "A 3' rich element in the 5' and translated region is necessary for the
RT translation of p27 mRNA.";
RL Mol. Cell. Biol. 20:5947-5959(2000);
DR EMBL: AY004255; AAF88142.1;
DR InterPro: IPR003175; CDI: 1;
DR Pfam: PF02244; CDI: 1;
SQ SEQUENCE 198 AA, 22012 MW, 51400142626246 CRC64;

Query Match 97.18; Score 374; DB 4; Length 198;
Best Local Similarity 95.58; Pred. No. 4.9e 44;

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Query Match 96.18; Score 369; DB 4; Length 158;
Best Local Similarity 94.06; Pred. No. 8.6e 44;
Matches 64; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKSAACRRLTCTVQVHRLTLEKLEKPEKMEASQKKNKFFQNIKPLKRYVQVVER 60
DB 22 DHPKSAACRRLTCTVQVHRLTLEKLEKPEKMEASQKKNKFFQNIKPLKRYVQVVER 60
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 4
QY 045806 PRELIMINARY: PFI: 158 AA.
AC 045806:
DI 01 JUN 1998 (TEMBLrel, 06, Created)
DI 01 JUN 1998 (TEMBLrel, 06, Last sequence update)
DI 01 DEC 2001 (TEMBLrel, 19, Last annotation update)
DE p27 Kip1 protein (Fragment).
CN p27 KIP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Lox10-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE 96140757; PubMed 8557269;
KA Ferrando A.A., Balbin M., Pendas A.M., Vizoso F., Velasco G.;
ET Lopez-otin C.;
KA p27 Kip1 in primary breast carcinomas";
RL Hum. Genet. 97:91-94(1996);
DR EMBL: X84849; CAA59284.1;
DR InterPro: IPR003175; CDI: 1;
DR Pfam: PF02244; CDI: 1;
DR VANT 109 109 G - V.
FT NON_CODING 158 158
SQ SEQUENCE 158 AA, 17651 MW, D8672905BAZFL150 CRC64;

Query Match 96.18; Score 369; DB 4; Length 158;
Best Local Similarity 94.06; Pred. No. 8.6e 44;
Matches 64; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKSAACRRLTCTVQVHRLTLEKLEKPEKMEASQKKNKFFQNIKPLKRYVQVVER 60
DB 22 DHPKSAACRRLTCTVQVHRLTLEKLEKPEKMEASQKKNKFFQNIKPLKRYVQVVER 60
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 5
QY 045806 PRELIMINARY: PFI: 148 AA.
AC 045806:
DI 01 OCT 2000 (TEMBLrel, 15, Created)
DI 01 OCT 2000 (TEMBLrel, 15, Last sequence update)
DI 01 DEC 2001 (TEMBLrel, 19, Last annotation update)
DE Cyclin-dependent kinase inhibitor p27Kip1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Lox10-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: HEPATOMA;
KA Li J., Wang W., Li, Yang A., Kuo Y., X.;
ET "Homo sapiens cyclin-dependent kinase inhibitor p27kip1 cDNA.";
RL Submitted (MAR 2000) to the EMBL/Genbank/DBJL databases;
DR EMBL: AF247511; AAF69497.1;
DR InterPro: IPR003175; CDI: 1;

```

DR Pfam: PF02234; CDI; 1.  
KW Kinase  
SQ SEQUENCE 198 AA; 22099 MW; 40E7D58901C9F3FA C6C64;  
  
Query Match  
Best Local Similarity 94.0%; Score 369; DB 4; Length 198;  
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DHPKPSACRNLFPGVNHHELTLDLEKHCRCRDMEASQKKNFDFONHKPLEGKRYEWOEVER 60  
Db 22 EHPYPSACRNLFPGVNHHELTLDLEKHCRCRDMEASQKKNFDFONHKPLEGKRYEWOEVER 61  
QY 61 GSLPEFY 67  
Db 82 GSLPEFY 88  
|||||  
  
RESULT 6  
Q9BUS6 PRELIMINARY; PRT; 198 AA.  
ID Q9BUS6;  
AC Q9BUS6;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE 01-MAP-2002 (TREMBLrel. 20, Last annotation update)  
DE Similar to cyclin-dependent kinase inhibitor 1b (p27, Kip1).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=CERVIX;  
RA Strausberg K.;  
PL Submitted (JAN-2001) to the EMBL GenBank/GenBank databases  
DR EMBL: B001471; AA001471 1;  
DR InterPro: IPR003175; CDI.  
DR Pfam: PF02234; CDI; 1.  
KW Cyclin Kinase.  
SQ SEQUENCE 198 AA; 22031 MW; 110R049910C9F3ED C6C64;  
  
Query Match  
Best Local Similarity 94.0%; Score 369; DB 4; Length 198;  
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DHPKPSACRNLFPGVNHHELTLDLEKHCRCRDMEASQKKNFDFONHKPLEGKRYEWOEVER 60  
Db 22 EHPYPSACRNLFPGVNHHELTLDLEKHCRCRDMEASQKKNFDFONHKPLEGKRYEWOEVER 61  
QY 61 GSLPEFY 67  
Db 82 GSLPEFY 88  
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RESULT 7  
Q9BEA5 PRELIMINARY; PRT; 172 AA.  
ID Q9BEA5;  
AC Q9BEA5;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE p27Kip1 degradation-resistant isoform (Fragment).  
GN P27KIP1.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21063196; PubMed=11115398.  
RA Hirano K., Hirano M., Zeng Y., Nishimura J., Hara K., Mita K.,  
Nawata H., Kanai H.;  
RT "Cloning and functional expression of a degradation-resistant novel  
isoform of p27Kip1."  
PL Biochem 1 353:51-57(2001).  
DR EMBL: AB031957; BAB39727.1;  
DR EMBL: AB031955; BAB39725.1;  
DR EMBL: AB031956; BAB39726.1;  
DR InterPro: IPR003175; CDI.  
DR Pfam: PF02234; CDI; 1.  
SQ SEQUENCE 198 AA; 22201 MW; E5B01D225E5B015F C6C64;  
  
Query Match  
Best Local Similarity 95.8%; Score 368; DB 6; Length 198;  
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DHPKPSACRNLFPGVNHHELTLDLEKHCRCRDMEASQKKNFDFONHKPLEGKRYEWOEVER 60  
Db 22 EYKPSACRNLFPGVNHHELTLDLEKHCRCRDMEASQKKNFDFONHKPLEGKRYEWOEVER 81  
QY 61 GSLPEFY 67  
Db 82 GSLPEFY 88  
|||||  
  
RESULT 9  
Q90YX4 PRELIMINARY; PRT; 179 AA.  
ID Q90YX4;  
AC Q90YX4;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAP-2002 (TREMBLrel. 20, Last annotation update)  
DE p27-like cyclin-dependent kinase inhibitor  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RL Biochem. J. 353:51-57(2001).  
DR EMBL: AB031958; BAB39728.1;  
DR InterPro: IPR002047; AKH.  
DR InterPro: IPR003175; CDI.  
DR Pfam: PF02234; CDI; 1.  
DR PPSCITE, PS0256, AKH, UNKNWN\_1.  
FT NON\_TER 1 1  
SQ SEQUENCE 172 AA; 15348 MW; 985E2F3C8B0C4A46E C6C64;  
  
Query Match  
Best Local Similarity 95.8%; Score 368; DB 6; Length 172;  
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DHPKPSACRNLFPGVNHHELTLDLEKHCRCRDMEASQKKNFDFONHKPLEGKRYEWOEVER 60  
Db 14 EYKPSACRNLFPGVNHHELTLDLEKHCRCRDMEASQKKNFDFONHKPLEGKRYEWOEVER 73  
QY 61 GSLPEFY 67  
Db 74 GSLPEFY 80  
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RESULT 8  
Q9BDC3 PRELIMINARY; PRT; 198 AA.  
ID Q9BDC3;  
AC Q9BDC3;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE P27Kip1.  
GN P27KIP1.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21063196; PubMed=11115398;  
RA Hirano K., Hirano M., Zeng Y., Nishimura J., Hara K., Mita K.,  
Nawata H., Kanai H.;  
RT "Cloning and functional expression of a degradation-resistant novel  
isoform of p27Kip1."  
PL Biochem 1 353:51-57(2001).  
DR EMBL: AB031957; BAB39727.1;  
DR EMBL: AB031955; BAB39725.1;  
DR EMBL: AB031956; BAB39726.1;  
DR InterPro: IPR003175; CDI.  
DR Pfam: PF02234; CDI; 1.  
SQ SEQUENCE 198 AA; 22201 MW; E5B01D225E5B015F C6C64;  
  
Query Match  
Best Local Similarity 94.0%; Score 368; DB 6; Length 198;  
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DHPKPSACRNLFPGVNHHELTLDLEKHCRCRDMEASQKKNFDFONHKPLEGKRYEWOEVER 60  
Db 22 EYKPSACRNLFPGVNHHELTLDLEKHCRCRDMEASQKKNFDFONHKPLEGKRYEWOEVER 81  
QY 61 GSLPEFY 67  
Db 82 GSLPEFY 88  
|||||  
  
RESULT 9  
Q90YX4 PRELIMINARY; PRT; 179 AA.  
ID Q90YX4;  
AC Q90YX4;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAP-2002 (TREMBLrel. 20, Last annotation update)  
DE p27-like cyclin-dependent kinase inhibitor  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





146 94 Y 94

SEARCHED BY: JEFFREY M. J. 06/02/03 17:01:11  
DATE: 06/02/03 17:01:11



Genome version 5.1.6  
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OM protein - protein search, using sw mod-1

Run on: May 30, 2003, 08:51:11 Search time 37.075 seconds  
(without alignment)  
606 682 Million cell updates/sec

Title: US-09-865-018b-6

Perfect score: 952

Sequence: 1 MSNFRVSVSSPSTFEMAPQ

Scoring table: BLOSUM62

Gap 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	952	100.0	178	16	AA199131 Mink kipl, p27-kipl
2	952	100.0	178	17	AA1992707 Mink p27 Kipl part
3	952	100.0	178	19	AA1992719 Partial 27 kDa pro
4	910	95.6	198	23	AA1991589 Porcine p27Kipl po
5	870	91.4	194	20	AA1994930 Amino acid sequenc
6	870	91.4	198	17	AA1994704 Human p27 kipl. H
7	870	91.4	198	19	AA1992717 27 kDa protein inh
8	870	91.4	198	19	AA1994888 Amino acid sequenc
9	870	91.4	198	20	AA1990768 K1/KIP protein p2
10	870	91.4	198	21	AA1997523 Human p27 protein

11	870	91.4	198	21	AA1996052 Human cyclin depen
12	870	91.4	198	21	AA1996066 Human cyclin depen
13	870	91.4	198	21	AA1994400 Human p27(Kipl) ki
14	870	91.4	198	22	AA1994449 Amino acid sequenc
15	870	91.4	198	22	AA1994409 Human p27 protein.
16	870	91.4	198	23	AA1994780 p27-Kipl Homo sa
17	867	91.1	198	21	AA1994007 Human mutant cycli
18	865	90.9	197	18	AA1993534 CDK inhibitory fus
19	865	90.9	197	18	AA1993534 Human p27-p16 fusi
20	865	90.9	197	21	AA1993525 Human W3 protein s
21	865	90.9	197	21	AA1993525 Antiproliferative
22	865	90.9	197	21	AA1993525 Angiogenesis inh
23	863	90.7	198	16	AA1993133 Human Kipl, p27-ki
24	860	90.3	365	18	AA1993530 CDK inhibitory fus
25	860	90.3	365	20	AA1995107 Human p16p27 fusio
26	860	90.3	365	20	AA1995096 Human p16p27 fusio
27	860	90.3	365	21	AA1997529 Human W6 protein s
28	860	90.3	365	21	AA1996044 Antiproliferative
29	860	90.3	365	21	AA1996071 Angiogenesis inh
30	860	90.3	380	18	AA1993535 CDK inhibitory fus
31	860	90.3	380	20	AA1995095 Human p16(GS)p27 f
32	860	90.3	380	21	AA1997528 Human W5 protein s
33	860	90.3	380	21	AA1996043 Antiproliferative
34	860	90.3	380	21	AA1996070 Angiogenesis inh
35	855	89.8	197	16	AA1993132 Murine kipl, p27-k
36	855	89.8	197	17	AA1992708 Mouse p27 Kipl. M
37	855	89.8	197	19	AA1992718 27 kDa protein inh
38	855	89.8	197	20	AA1998819 Mouse wild type p2
39	855	89.8	197	20	AA1998847 Murine wild type p
40	855	89.8	197	22	AA1994850 Amino acid sequenc
41	854	89.6	365	21	AA1997527 Human W4 protein s
42	854	89.6	365	21	AA1997527 Antiproliferative
43	853	89.6	365	21	AA1996069 Angiogenesis inh
44	854	89.6	365	20	AA1993530 Mouse p27 mutant p
45	854	89.6	365	20	AA1993530 Murine mutant p27

ALIGNMENTS

RESULT 1

AA199131 standard; protein, 178 AA.

AA199131:

27-FEB-1996 (first entry)

Mink kipl, p27 kipl or p27, cyclin E-Cdk2 activation inhibitor.

Mink kipl, p27-kipl, p27, cyclin E-Cdk2 complex, cancer,

activation inhibitor, hyperplasia, cyclin dependent kinase,

diagnosis, hyperproliferative disorder, abut, partial protein.

Mustela vison.

Key Peptide Location/Qualifiers

31..43 /note= "obtd. from purified kipl, and

used to design degenerate oligo-

nucleotide PCR primer"

Peptide 74..79 /note= "obtd. from purified kipl, and

used to design degenerate oligo-

nucleotide PCR primer"

Peptide 83..96 /note= "obtd. from purified kipl"

Peptide 114..122 /note= "obtd. from purified kipl"

Peptide 135..147 /note= "obtd. from purified kipl"

W09518824-A1.

```

XX 03 JUN 1996.
XX 03 JUN 1996. 9405 US0764.
XX 15 JUL 1994. 9405 02750602.
XX 03 JUN 1994. 9405 01700415.
XX (HUTCHINSON) CANCER RES. CENT. PREL.
XX (SLOK) CYCLIN KINETIC INHIBITOR FOR CANCER RESEARCH.
XX KOTI A. Massague J. Polyak K. Roberts JM.
XX WILKINS J. 255067/46.
XX Nucleo protein p27 inhibits activation of a cyclin E-cdk2 complex
XX useful for treatment of hyperproliferative disorders, esp. cancer,
XX hyperplasia or ulcers.
XX Disclosure: Fig 9A; 121pp; English.
XX AAK795.01 p27/159 are respective mink, murine and human kipl (p27/kipl
XX or p27) partial proteins. p27 inhibits the activation of the cyclin
XX E-cdk2 (cyclin dependent kinase) complex. A p27 which inhibits or
XX enhance the ability of p27 to inhibit the activation of cyclin
XX E-cdk2 can be used to treat hyperproliferative disorders, esp.
XX cancer, hyperplasia or ulcers. Diagnosis of hyperproliferative
XX disorders, esp. human cancer, can be achieved by detecting a p27
XX mutation in the cells of the patient. The disorder can be treated
XX using a pharmaceutical compsn. comprising a recombinant virus
XX confg. a nucleic acid mol. encoding p27.
XX Sequence 178 AA:
SQ
Query Match. 100.0% Score 952. DB 16; Length 178;
Best Local Similarity 100.0% Prod. No. 436 95;
Matches 178; Conservation 0; Mismatches 0; Gaps 0;
QY 1 MSNVRVNSISLEPMARQAYTKISACRNLEPGYNHEELRDLKRRHMEASQKRW 60
DB 1 MSNVRVNSISLEPMARQAYTKISACRNLEPGYNHEELRDLKRRHMEASQKRW 60
QY 61 NPTQNHREPLKRYKRWQVEKSSLEFVYRGRPRPRKACVACQSSAVSTPGAVPLMG 120
DB 61 NPTQNHREPLKRYKRWQVEKSSLEFVYRGRPRPRKACVACQSSAVSTPGAVPLMG 120
QY 121 SQANSEDLHVLQKIDALNQAALAQVGLGKKKFAHDS QNRKAPLENNVDSS 178
DB 121 SQANSEDLHVLQKIDALNQAALAQVGLGKKKFAHDS QNRKAPLENNVDSS 178
P45911.4
AAW29719
ID AAW29719 standard; Protein: 178 AA
XX
XX AAW29719;
XX
XX 27 OCT 1998 (first entry)
XX
XX Partial 27 kDa protein inhibitor activation of cyclin E-cdk2 complex.
XX
XX Mink p27 Kipl partial sequence.
XX
XX p27 protein Kipl; cyclin E-cdk2 cell proliferation; ulcers;
XX cancer; hyperplasia; diagnosis; therapy.
XX
XX Mustela SP.
XX
XX W09834121 A2
XX
XX 06 AUG 1998.
XX
XX 05 FEB 1998; 99W0 US018994.
XX
XX 05 FEB 1997; 97US 0740092.
XX
XX (HUTCHINSON) CANCER RES. CENT. PREL.

```

XX Porter PL, Roberts JM;  
PI  
XX WPI: 1998-437612/37.  
DR N-PSDB: AAV47519.  
XX  
XX Assays for protein p27 inhibiting activation of cyclin E-Cdk2  
PT complex - useful for, e.g. diagnosis and prognosis of cancer,  
PT especially breast carcinoma  
XX  
XX Disclosure: Fig 13B; 105pp; English.  
PS  
XX The present sequence represents a partial 27 kDa protein (p27 or Kip1)  
CC which inhibits the activation of a cyclin E-cyclin-dependent kinase2  
CC (Cdk2) complex. A reduced relative level of Kip1 is indicative of a  
CC hyperproliferative disease (particularly cancer, especially breast  
CC carcinoma) and also is prognostic for increased risk of death and/or  
CC recurrence of cancer (and may be used to determine suitable treatments).  
CC Agents that affect the activity of Kip1 can be used to treat  
CC hyperproliferative conditions, e.g. to stimulate tissue or organ repair  
CC or to establish cell cultures.  
XX  
SQ Sequence 178 AA;

Query Match 100.0%; Score 952; DB 19; Length 178;  
Best Local Similarity 100.0%; Pred. No. 3.8e-95;  
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSNVVNSGSPSLERMDARQAEYKPKPSACPNLFGPVNHEELTDLEKHPDMEASQKWK 60  
DB 1 MSNVVNSGSPSLERMDARQAEYKPKPSACPNLFGPVNHEELTDLEKHPDMEASQKWK 60  
QY 61 NFDQNHKPLEGKYEWQVEKSLPEFFYYPPPPKCAKVPAGQSVWSSTPQAVPLMG 120  
DB 61 NFDQNHKPLEGKYEWQVEKSLPEFFYYPPPPKCAKVPAGQSVWSSTPQAVPLMG 120  
QY 121 SCANSEDLHLVDQKIDTADNAGLAEOCTGIRKRPATDDSSPQNKRRNTEENVSDGS 178  
DB 121 SCANSEDLHLVDQKIDTADNAGLAEOCTGIRKRPATDDSSPQNKRRNTEENVSDGS 178

RESULT 4  
AAM51589  
ID AAM51589 standard; Protein: 198 AA.  
XX  
AC AAM51589;  
XX

DT 01-FEB-2002 (first entry)  
XX

DE Porcine p27Kip1 polypeptide #2.  
XX

XX P1; antiarteriosclerosis; cytostatic; gene therapy; p27Kip1;  
KW proteasome decomposition resistance; cancer; arteriosclerosis.  
XX

XX Sus scrofa.  
XX

XX JP2001258561-A.  
XX

XX 25 SEP-2001.  
XX

XX 17-MAR-2000; 2000JP-0076840.  
XX

XX 17-MAR-2000; 2000JP-0076840.  
XX

XX (UYKY-) UNIV KYUSHU.  
XX

XX WPI: 2002-003329/01  
DR

XX N-PSDB: ABA01080.  
XX

XX Nucleic acid and amino acid sequence for showing resistance against  
PT proteasome decomposition, comprises a new p27Kip1 molecular species -  
XX

XX Disclosure: Page 8-9; 12pp; Japanese.  
PS

XX The invention relates to a novel p27Kip1 polynucleotide and protein  
CC The p27Kip1 protein shows resistance to proteasome decomposition  
CC and can be used in the treatment of cancers and arteriosclerosis. The  
CC invention also relates to a recombinant vector containing the  
CC polynucleotide, and to a transformant containing the recombinant  
CC vector. The present sequence is a p27Kip1 polypeptide.  
XX

SQ Sequence 198 AA;

Query Match 95.6%; Score 910; DB 23; Length 198;  
Best Local Similarity 95.5%; Pred. No. 1.1e-90;  
Matches 170; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MSNVVNSGSPSLERMDARQAEYKPKPSACPNLFGPVNHEELTDLEKHPDMEASQKWK 60  
DB 1 MSNVVNSGSPSLERMDARQAEYKPKPSACPNLFGPVNHEELTDLEKHPDMEASQKWK 60  
QY 61 NFDQNHKPLEGKYEWQVEKSLPEFFYYPPPPKCAKVPAGQSVWSSTPQAVPLMG 120  
DB 61 NFDQNHKPLEGKYEWQVEKSLPEFFYYPPPPKCAKVPAGQSVWSSTPQAVPLMG 120  
QY 121 SCANSEDLHLVDQKIDTADNAGLAEOCTGIRKRPATDDSSPQNKRRNTEENVSDGS 178  
DB 121 SCANSEDLHLVDQKIDTADNAGLAEOCTGIRKRPATDDSSPQNKRRNTEENVSDGS 178

RESULT 5  
AAW94930  
ID AAW94930 standard; Protein: 194 AA.  
XX

AC AAW94930;  
XX

DT 11-MAY-1999 (first entry)  
XX

DE Amino acid sequence of p27 protein.  
XX

XX Vascular proliferative disease; p27 protein; fusion protein; restenosis;  
KW arteriosclerosis; angiogenesis; smooth muscle; cell proliferation; TK;  
KW thymidine kinase; gancyclovir; GCV.  
XX

XX Homo sapiens.  
XX

XX WC9903508-A2.  
XX

XX 28-JAN-1999.  
XX

XX 21 JUL-1998; 98WO US15025.  
XX

XX 21-JUL-1997; 97US-0897333.  
XX

XX (UNMI) UNIV MICHIGAN.  
XX

XX Nabel EG, Nabel GJ;  
XX

XX WPI: 1999-131876/11.  
XX

XX N-PSDB: AAX17752.  
XX

XX Treating vascular proliferative disease with p27 gene - used  
PT particularly to treat restenosis, arteriosclerosis and angiogenesis  
PT or to inhibit intimal smooth muscle cell growth  
XX

XX Example 1; Fig 5; 40pp; English.  
PS

XX The invention relates to a method of treating vascular proliferative  
CC diseases. The method comprises in vivo administration of a gene encoding  
CC p27; or fusion proteins consisting of p27 linked to a second polypeptide.  
CC p27 is used to treat, or prevent, restenosis (coronary or peripheral),  
CC arteriosclerosis or angiogenesis, or generally to inhibit growth of  
CC intimal smooth muscle cells. The method is based on the discovery that  
CC p27 functions in arteries to control response to acute injury and cell  
CC proliferation. Its (over)expression is sufficient to inhibit growth of  
CC vascular smooth muscle cells in vivo. Arresting cells with p27 renders

cc them transiently insensitive to thymidine kinase (TK)/ganciclovir (GCV)  
 cc mediated killing, prolonging their life and duration of TK expression;  
 cc so increasing transport of phosphorylated GCV to host under cells;  
 cc increasing the bystander effect. The present sequence represents a  
 cc p27 protein.

XX  
 SS Sequence 194 AA;

Query Match 91.4%; Score 870; ID: 20; Length 194;  
 best local similarity 91.0%; Prod. No. 3,60,86;  
 Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
 07 1 MSNVEVSESSLEEMAFQAVIKESATRELEFVNHLEELRLEKRRMEEAASQKWK 60  
 14 1 MSNVEVSESSLEEMAFQAVIKESATRELEFVNHLEELRLEKRRMEEAASQKWK 60  
 09 61 NTFQNHKLEKLEFVSESSLEEMAFQAVIKESATRELEFVNHLEELRLEKRRMEEAASQKWK 120  
 14 61 NTFQNHKLEKLEFVSESSLEEMAFQAVIKESATRELEFVNHLEELRLEKRRMEEAASQKWK 120  
 09 121 SVANSDEHIVCKIDIAINQAGALQETTERKRAIDERSQNKANRTEENVSDS 178  
 14 121 SVANSDEHIVCKIDIAINQAGALQETTERKRAIDERSQNKANRTEENVSDS 178  
 09 141 AVANSDEHIVCKIDIAINQAGALQETTERKRAIDERSQNKANRTEENVSDS 178  
 14 141 AVANSDEHIVCKIDIAINQAGALQETTERKRAIDERSQNKANRTEENVSDS 178

RESILI  
 AAR92709  
 14 AAR92709 standard; Protein: 196 AA;

XX  
 AC AAR92709;  
 XX  
 XX 12 JUL 1996 (first entry)  
 14 Human p27 Kip1;  
 XX  
 XX p27 protein Kip1, cyclin E, CDK2, cell proliferation, growth;  
 KW cancer; hyperplasia; diagnosis; therapy;  
 KW  
 XX Homo sapiens;  
 XX  
 XX W 060140 A1;  
 XX  
 XX 01 FEB 1996;  
 XX  
 XX 01 JUN 1996; 96W00501694;  
 XX  
 XX 15 JUL 1996; 94US 0276085;  
 XX  
 XX (HIT) ) HUTCHINSON CANCER RES CTR, FRED;  
 14 (SHK) ) SLOAN KETTERING INST CANCER RES;

XX  
 14 Kell A, Massague J, Polyak K, Roberts JM;  
 XX  
 14 WEL 1996 19565471;  
 14 N 15506; AAL16666;  
 XX  
 14 p27 is inhibitor of cyclin E-Cdk2 complex activation and arrests  
 14 which enhance and inhibit its activity, useful for treating  
 14 hyperproliferative and hypoproliferative disorders  
 XX  
 14 Disclosure: Fig 15a b; 12pp; English;  
 XX

cc A cDNA clone (AAL16666) derived from human kidney codes for a 27  
 cc Kip protein, p27 Kip1 (AAR92709), that is capable of binding to  
 cc and inhibiting the activation of a cyclin E-Cdk2 complex. Human  
 cc Kip1 shows a high degree of homology to murine (AAR92707) and mouse  
 cc (AAR92708) Kip1 proteins, and the N terminal half of the protein shows  
 cc significant homology to cupbowen-1. Kip1 shows ask inhibitory  
 cc activity and prevents cdk2 activation. Overexpression inhibits  
 cc cell entry to the S phase. Kip1 can be produced by expression of  
 cc the cDNA clone in cultured cells. It can be used in *in vitro*  
 cc assays to screen agents that affect p27 activity, and in methods  
 cc for the diagnosis and treatment of hyperproliferative disorders.

cc cell cycle, and hyperproliferative disorders, and cancer and  
 cc hyperplasia.

XX  
 SS Sequence 196 AA;

Query Match 91.4%; Score 870; ID: 17; Length 196;  
 best local similarity 91.0%; Prod. No. 3,60,86;  
 Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
 07 1 MSNVEVSESSLEEMAFQAVIKESATRELEFVNHLEELRLEKRRMEEAASQKWK 60  
 14 1 MSNVEVSESSLEEMAFQAVIKESATRELEFVNHLEELRLEKRRMEEAASQKWK 60  
 09 61 NTFQNHKLEKLEFVSESSLEEMAFQAVIKESATRELEFVNHLEELRLEKRRMEEAASQKWK 120  
 14 61 NTFQNHKLEKLEFVSESSLEEMAFQAVIKESATRELEFVNHLEELRLEKRRMEEAASQKWK 120  
 09 121 SVANSDEHIVCKIDIAINQAGALQETTERKRAIDERSQNKANRTEENVSDS 178  
 14 121 SVANSDEHIVCKIDIAINQAGALQETTERKRAIDERSQNKANRTEENVSDS 178  
 09 141 AVANSDEHIVCKIDIAINQAGALQETTERKRAIDERSQNKANRTEENVSDS 178  
 14 141 AVANSDEHIVCKIDIAINQAGALQETTERKRAIDERSQNKANRTEENVSDS 178

RESILI  
 AAR92717  
 14 AAR92717 standard; Protein: 196 AA;

XX  
 AC AAR92717;  
 XX  
 XX 27 OCT 1996 (first entry)  
 14 27 Kip protein, inhibitor of activation of cyclin E-Cdk2 complex;  
 14  
 14 27 Kip protein, p27, Kip1, cyclin E, CDK2, cell cycle, cancer;  
 KW cyclin E-cyclin-dependent kinase2 complex; hyperproliferative disease;  
 KW recurrence; treatment; human;  
 XX  
 XX Homo sapiens;  
 XX  
 XX W 060141 A2;  
 XX  
 XX 01 AUG 1996;  
 XX  
 XX 01 FEB 1996; 96W00501694;  
 XX  
 XX 01 FEB 1997; 94US 0276082;  
 XX  
 XX (HIT) ) HUTCHINSON CANCER RES CTR, FRED;

XX  
 14 Porter DL, Roberts JM;  
 XX  
 14 WEL 1996 40612771;  
 14 N 15506; AAR92717;  
 XX  
 14 Assays for protein p27 inhibiting activation of cyclin E-Cdk2  
 14 complex useful for cell diagnosis and prognosis of cancer,  
 14 especially breast carcinoma

XX  
 14 Claim 14; Fig 15a; 10pp; English;  
 XX  
 14 The present sequence represents a 27 kDa protein (p27 or Kip1) which  
 14 inhibits the activation of a cyclin E-cyclin dependent kinase2 (cdk2)  
 14 complex. A reduced relative level of Kip1 is indicative of a  
 14 hyperproliferative disease (particularly cancer, especially breast  
 14 carcinoma) and also is proposed for increased risk of death and/or  
 14 recurrence of cancer (and may be used to determine suitable treatments).

cc Agents that affect the activity of Kip1 can be used to treat  
 cc hyperproliferative conditions, used to stimulate tissue or organ repair  
 cc or to establish cell cultures.

XX  
 SS Sequence 196 AA;  
 Query Match 91.4%; Score 870; ID: 16; Length 196;  
 best local similarity 91.0%; Prod. No. 3,60,86;

Matches 162; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSNVRVSNQSPSIFMVARQAHYPRPSACRNIFGPVNHHEELIFGLKHKHPYDMEEASQPKW 60  
 DB 1 MSNVRVSNQSPSIFMVARQAHYPRPSACRNIFGPVNHHEELIFGLKHKHPYDMEEASQPKW 60  
 QY 61 NFEQGNHKLPLEKYEWEVEKESLSPEFYRPPPPKACVKVPAQESQVSGTQAVPLMG 120  
 DB 61 NFEQGNHKLPLEKYEWEVEKESLSPEFYRPPPPKACVKVPAQESQVSGTQAVPLMG 120  
 QY 121 SQANSEDTLHVQKTDITADNQAAGLACQCTGIRKRPATDDSSQNKRNKRNTEENVSDGS 178  
 DB 121 APANSEDTLHVQKTDITADNQAAGLACQCTGIRKRPATDDSSQNKRNKRNTEENVSDGS 178

## RESULT 8

AAW46888 standard; Protein: 198 AA.

XX AC AAW46888;

XX DT 15-JUN-1998 (first entry)

XX DE Amino acid sequence of the p27KIP1 protein.

XX KW E7 oncoprotein; proliferative state; HPV; Kinase activity;

XX KW cyclin/cyclin-dependent kinase; p21CIP1; interaction; inactivation;

XX KW cyclin/cyclin-dependent kinase inhibitor.

XX OS Homo sapiens.

XX PN US5736318-A.

XX PD 07-APR-1998.

XX PF 17-MAR-1995; 95US-0406248.

XX PR 17-MAR-1995; 95US-0406248.

XX PA (HARD ) HARVARD COLLEGE.

XX PA (HARD ) UNIV HARVARD.

XX PI Jones DL, Munger K;

XX PI WPI: 1998-239292/21.

XX DR N-PSDB; AAV16719.

XX PT Evaluation of proliferative state of cells transformed with human  
 PT papilloma virus - by determining cyclin-dependent kinase activity  
 PT induced by E7 onco-protein

XX PS Disclosure; Columns 17-18; 14pp; English.

XX CC The present sequence represents a p27KIP1 protein, which is part of a  
 CC family of small cyclin-dependent kinase inhibitors. The proliferative  
 CC state of a cell transformed with human papillomavirus (HPV) can be  
 CC evaluated in the following manner. Cyclin/cyclin dependent kinase  
 CC complexes containing protein p27KIP1 are isolated from the transformed  
 CC cell, and the HPV E7 onco-protein (AAW46886) added to the isolated  
 CC protein. Cyclin/cyclin-dependent kinase complexes are isolated from an  
 CC untransformed cell that is substantially homogenic with the transformed  
 CC cell, and the HPV E7 onco-protein added. The kinase activities of the 2  
 CC samples are measured, where a proliferating transformed cell has a  
 CC greater kinase activity than the untransformed cell. The method is  
 CC used for determining the extent of interaction and/or inactivation  
 CC between a cyclin/cyclin-dependent kinase inhibitor and the HPV E7  
 CC oncoprotein and thus evaluating the proliferative state of a transformed  
 CC cell.

XX SQ Sequence 198 AA;

Query Match 91.4%; Score 870; DB 19; Length 198;  
 Best Local Similarity 91.0%; Pred No. 3 6a-86;

Matches 162; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSNVRVSNQSPSIFMVARQAHYPRPSACRNIFGPVNHHEELIFGLKHKHPYDMEEASQPKW 60  
 DB 1 MSNVRVSNQSPSIFMVARQAHYPRPSACRNIFGPVNHHEELIFGLKHKHPYDMEEASQPKW 60  
 QY 61 NFEQGNHKLPLEKYEWEVEKESLSPEFYRPPPPKACVKVPAQESQVSGTQAVPLMG 120  
 DB 61 NFEQGNHKLPLEKYEWEVEKESLSPEFYRPPPPKACVKVPAQESQVSGTQAVPLMG 120  
 QY 121 SQANSEDTLHVQKTDITADNQAAGLACQCTGIRKRPATDDSSQNKRNKRNTEENVSDGS 178  
 DB 121 APANSEDTLHVQKTDITADNQAAGLACQCTGIRKRPATDDSSQNKRNKRNTEENVSDGS 178

## RESULT 9

AAW00768 standard; Protein: 198 AA.

XX AC AAY00768;

XX DT 14-MAY-1999 (first entry)

XX DE CK1/KIP protein p27.

XX KW CK1/KIP protein; p27 protein; cyclin kinase inhibitor; cancer;

XX KW hyperproliferative disorder.

XX OS Homo sapiens.

XX PN WO9904238-A2.

XX PD 28-JAN-1999.

XX PF 14-JUL-1998; 98WO-US14566.

XX PR 15-JUL-1997; 97US-0893276.

XX XX (DEAC-) DEACONESS HOSPITAL.

XX PA (MITO-) MITOTIX INC.

XX PI Draetta G, Loda M, Pagano M, Rolfe M;

XX PI WPI: 1999-132426/11.

XX DR N-PSDB; AAX21817.

XX PT Methods for diagnosis and prognosis of hyperproliferative disorders  
 PT - by determining the level of cyclin kinase inhibitor protein(s),  
 PT particularly p27

XX PS Claim 18; Page 36 37; 53pp; English.

XX CC This sequence is the cyclin kinase inhibitor (CKI) protein p27. The  
 CC invention relates to a method for diagnosing a hyperproliferative  
 CC disorder, associated with the destabilisation of a CKI protein in cells  
 CC of a patient, comprises: (i) ascertaining the CKI protein level in a  
 CC sample of patient cells; and (ii) diagnosing the presence or absence of a  
 CC hyperproliferative disorder by utilising the ascertained CKI protein  
 CC level, where a reduced CKI protein level, relative to a normal control  
 CC cell sample, correlates with the presence of a hyperproliferative  
 CC disorder. The methods are useful for diagnosing disorders associated with  
 CC hyperproliferation, evaluating their aggressiveness and/or rate of  
 CC recurrence and as prognosis for evaluating a cancer patient's risk of  
 CC death from the observations. Treatment can be applied on the basis of  
 CC the patient's risk of death and/or recurrence of the cancer. The  
 CC diagnostic methods may also be employed as follow-up to treatment,  
 CC e.g. quantitation of the level of p27 protein may be indicative of the  
 CC effectiveness of current or previously employed cancer therapies as well  
 CC as the effect of these therapies upon patient prognosis. The methods and  
 CC reagents allow the detection of loss of p27 protein from a cell in order  
 CC to diagnose and phenotype proliferative disorders arising from  
 CC tumorigenic transformation of cells, or other hyperplastic or neoplastic  
 CC transformation processes as well as differentiative disorders such as



The present sequence is that of human p27, a cyclin dependent kinase inhibitor (CKI) that inhibits smooth muscle cell proliferation. A claimed method for inhibiting smooth muscle cell hyperproliferation involves transducing smooth muscle cells with a replication-deficient recombinant adenovirus that lacks a functional E1 region and a functional E4 region, and comprises a transgene encoding a CDKi. The CDKi is selected from an INK4 family protein such as human p16, a CIP/KIP family protein such as p27, active fragments of these, or fusion proteins comprising (active fragments of) an INK4 family protein and a CIP/KIP family protein (see AAY96046 and AAY96049). The method is used to inhibit mammalian smooth muscle cell hyperproliferation induced by injury caused by angioplasty, vessel placement or vein grafting. It is useful for treating vascular pathologies, e.g., restenosis. Also claimed are recombinant lentiviruses encoding CDKis.

Sequence: 198 AA:

Query Match: 91.4%, Score: 879, E-Value: 1e-21, Length: 198,  
Best Local Similarity: 91.0%; Pred No.: 3,6e-86;  
Matches: 162; Conservative: 7; Mismatches: 9; Indels: 0; Gaps: 0;

QY 1 MSWVSVSGSFSLERMDACAEYVPSPCFNIFGVNHIELTPLEKERFMEEFASQPKW 60  
DB : |||||  
QY 1 MSWVSVSGSFSLERMDAQAGRPSPACFNIFPVDFEETPLEKECFMEEASQPKW 60  
DB : |||||  
QY 61 NFDQNHKGTECKYEWGFEVKSTIEFFYPPEPPKGCACKVFACESCTVCNVFLMG 120  
DB : |||||  
QY 61 NFDQNHKGTECKYEWGFEVKSTIEFFYPPEPPKGCACKVFACESCTVCNVFLMG 120  
DB : |||||  
QY 121 SQANSDPHLVLPQITDAINLALAEQCTGIKKPFATIGSSPQNKPANKRFTENVSDGS 178  
DB : |||||  
QY 121 APANSEDTHLVDPKTDPSSQTGLAECAGIKKPAHICSSITUNKPANRFTENVSDGS 178  
DB : |||||

RESULT 12  
AAY96066 standard: Protein: 198 AA.  
AAY96066:  
05-DEC-2000 (first entry)

XX Human cyclin dependent kinase inhibitor p27.  
DE Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; human; p27;  
KW angiogenesis inhibitor; neoplasia; rheumatoid arthritis;  
KW endometriosis; psoriasis; vascular retinopathy; cytostatic;  
KW antiarthritis; antihematuric; gynecological; anticypsorietic;  
KW antiproliferative; gene therapy.  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH Domain 25..93  
FT /note= "CDK inhibitory domain"  
FT Domain 144..194  
FT /note= "GT domain"  
FT Peptide 152..166  
FT /note= "nuclear localisation signal"  
FT Modified-site 10..13  
FT /note= "o-phosphorylated; weak CKK phosphorylation site"  
FT Modified-site 178..181  
FT /note= "o-phosphorylated; phosphorylation site for proline-directed kinases"  
FT Modified-site 187..190  
FT /note= "o-phosphorylated; CKK phosphorylation consensus site"

WO2000052158 A1.  
08-SEP-2000.

```

XX      28-FEB-2000; 2000WO-USO4970.
XX
XX      01-MAP-1999;   qnrs-0123q74
XX PP      05-NOV-1999;   qnrs-0163q82
XX      09-DEC-1999;   99US-0457646.
XX
XX      (CELL-) CELL GENESYS INC.
XX      (MITO-) MITOTIX INC.
XX
XX      Patel S, McArthur J, Gyuris J;
XX
XX      WP1: 45900-5655q1/52.
XX N-PSDB; AAA50319.
XX
XX      Inhibiting angiogenesis and treating angiogenesis-associated
XX PT conditions, e.g neoplasia, psoriasis by transducing an endothelial
XX PT cell with a recombinant virus having a transgene encoding a cyclin
XX PT dependent kinase inhibitor -
XX
XX      Example 1: Page 127-128, 138pp, English.
XX
XX      The present sequence is that of human p27, a cyclin dependent
XX CC kinase inhibitor (CDKi) that inhibits angiogenesis. A claimed
XX CC method for inhibiting angiogenesis involves transducing an
XX CC epithelial cell with a transgene encoding (internally,
XX CC secretably) CDki. The delivery system for the transgene may be a
XX CC liposome or a recombinant virus. The CDki is preferably a protein
XX CC of the CIP/KIP family such as p27, a protein of the INK4 family
XX CC such as p16, active fragments of these proteins (e.g. amino acids
XX CC 25-35 or 12-178 of human p27), or a fusion of 2 CDki proteins such
XX CC as p27 and p16 (see AAY96088-80). The method is useful in treating
XX CC conditions associated with angiogenesis, e.g. neoplasia, rheumatoid
XX CC arthritis, endometriosis, psoriasis and vascular retinopathy
XX CC (claimed). Alternatively, the transgene is delivered to an
XX CC auxiliary cell, and is expressed by that cell such that the CDki is
XX CC released into the blood and contacts the target epithelial cell.
XX
XX      Sequence    198 AA:
XX
XX      Query Match          91.4%; Score 870; DB 21; Length 198;
XX      Best Local Similarity 91.0%; Pred. No. 3.6e-86;
XX      Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
XX
XX QY      1 MSNVFVSNGSPSLFPMDFQACYPKPSPACPNLFQGVNHEELTRDLEKHRRDMEEASQRKW 60
XX Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX      1 MSNVFVSNSGSPSLERMDAFQAEPKPSA-RNLFGPVDEELTKOLEKHCKUMEEASQRKW 60
XX
XX QY      61 NPFPNNHKFLDKXYEWVEKEKSLSLEFYPPKPKGACKVIAQSUVSGIKQAVPLMC 120
XX      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db      61 NPDFQNHPKPLECKYEWVEKEKSLSEFYPPRPPPKGACKVPQAQSDVSGSRPAAPLIG 120
XX
XX QY      121 SVANSSEDLVLVDKIDTALNAGLAEGCTGIKKKATDUSSPQNKANKTEENVSLGS 178
XX      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db      121 AVANSEDLVLDPFKTPDSLSUQLAQACAGIKKKATLUSSIQNKANKTEENVSLGS 178
XX
XX      RESULT 13
XX      AAY44400
XX ID      AAY44400 standard; Protein; 198 AA.
XX AC      AAY44400;
XX
XX XX      22-MAR-2000 (first entry)
XX
XX      Human p27(Kip1) kinase inhibitor protein.
XX
XX      p27(Kip1) kinase inhibitor protein; EMBL-12; p27(Kip1). FKBP-12 complex;
XX KW cytosolic drug-binding protein; yeast two hybrid assay system;
XX KW cell differentiation, apoptosis, neurodegeneration, tumorigenicity,
XX KW cell proliferation related disorder; arteriosclerosis, autoimmune disease;
XX KW transplant rejection, inflammation, allergy, cancer, viral infection,
XX KW membranous nephropathy; CDK; cyclin-dependent kinase.

```

XX Homo sapiens.  
 XX Key: Localization/Qualifiers  
 XX Residue: 45-198  
 XX Note: "Proy sequence that interacts with ERK12" 12"  
 XX W0906599 ALI.  
 XX 25 APR 1999.  
 XX 18 JUN 1999: 9906 0514059.  
 XX 18 JUN 1998: 9805-0094857.  
 XX (García J, Ceballos R, Cook R,  
 XX Nandabalan K, Yang M;  
 XX W01: 2000-116763/10.  
 XX N 0306, AA229564.  
 XX Rec complex of p27(Kip1) and p27(Kip1) for treatment, prevention and  
 XX diagnosis of, e.g., cancer and autoimmune disease -  
 XX Claim 1: Fig 1: 2app; English.  
 XX The present sequence is p27(Kip1) kinase inhibitor protein. This protein  
 XX regulates cell activity by inhibiting cyclin D1 and box associated kinase  
 XX activity, interaction between p27(Kip1) and ERK12 complex was detected  
 XX drug binding protein) to form a p27(Kip1)-p27(Kip1) complex was detected  
 XX using a modified yeast two hybrid assay system. This interaction is  
 XX used in regulating many cell functions, e.g., cell cycle progression,  
 XX differentiation, apoptosis, neurodegeneration, response to viral  
 XX infection, tumor necrosis factor (TNF) receptor 1 complex and its  
 XX corresponding nucleic acid sequence is used in diagnosis and treatment  
 XX of cell proliferation related disorders. Specified diseases are  
 XX attherosclerosis; autoimmune diseases (e.g., transplant rejection,  
 XX inflammation or allergy); neurodegeneration; cancer; membranous  
 XX nephropathy and viral infections.  
 XX Sequence: 198 AA;  
 XX  
 Query Match: 91.4%; Score: 870; DB: 21; Length: 198;  
 Best Local Similarity: 91.0%; Pred. No.: 4,66-86;  
 Matches: 162; Conservative: 7; Mismatches: 9; Indels: 0; Gaps: 0;  
 QY 1 MSNVVVSNGSISLERMARGAETIKTSACNRLNLTGVNHEE RDLKHKRDMEEASQPKW 60  
 DB 1 MSNVVVSNGSISLERMARGAETIKTSACNRLNLTGVNHEE RDLKHKRDMEEASQPKW 60  
 QY 61 NPEFQNHKPLGKAYEWGVEKSTGAEYEFSEETKACVKAQPELVAVTNGAVTMM 120  
 DB 61 NPEFQNHKPLGKAYEWGVEKSTGAEYEFSEETKACVKAQPELVAVTNGAVTMM 120  
 QY 121 SQANSETHLVQKTHFADNCAHLAQGTGIRKPAIDUSSEQNKRNKRNTEENVSDGS 178  
 DB 121 SQANSETHLVQKTHFADNCAHLAQGTGIRKPAIDUSSEQNKRNKRNTEENVSDGS 178  
 QY 121 AVANSETHLVQKTHFADNCAHLAQGTGIRKPAIDUSSEQNKRNKRNTEENVSDGS 178  
 DB 121 AVANSETHLVQKTHFADNCAHLAQGTGIRKPAIDUSSEQNKRNKRNTEENVSDGS 178  
 RESULT 15  
 AAB48309  
 10 AAB48309 standard; protein; 198 AA.  
 XX  
 XX AAB48309;  
 XX 02 APR 2001 (first entry)  
 XX Human p27 protein.  
 XX  
 XX S phase kinase associated protein; SKP1; SKP2; SKP3 like protein; ZP;  
 XX S phase kinase associated protein; SKP1; SKP2; SKP3 like protein; ZP;  
 XX Bcl-2; tumor; cytosolic.  
 XX

XX Homo sapiens.  
 XX 05A240965-B1.  
 XX 12 JUN 2001.  
 XX 29 JAN 1999: 9905 0240906.  
 XX 29 JAN 1999: 9905 0240906.  
 XX (SJOOD J, ST JHDE CHILDREN'S RES HOSPITAL,  
 XX Roussel ME, Smeeyne R, Zindy F, Cunningham JJ;  
 XX W01: 2001-421442/45.  
 XX N 0306, AA283326.  
 XX New knockout mouse having a genome comprising a homozygous disruption  
 XX of both p19 INK43 and p27 KIP1 genes, useful in animal models studying  
 XX motor disorders having symptoms that include bradykinesia and  
 XX proprioceptive abnormalities  
 XX Disclosure: Columns 31-34; 24pp; English.  
 XX The present sequence represents a human p27 KIP1 polypeptide. The  
 XX specification describes a knockout mouse whose genome is manipulated  
 XX to comprise a homozygous disruption of both the p19 INK43 and p27 KIP1  
 XX genes, where homozygous disruption of these genes results in the knockout  
 XX mouse exhibiting a phenotype of proprioceptive abnormalities, or  
 XX proceeds to the expression of functional p19 INK43 and p27 KIP1 proteins.  
 XX The knockout mouse and cells may be used to identify potential  
 XX modulator of cell growth and more particularly neuronal growth. The  
 XX knockout mouse is useful as animal model for study of motor disorders  
 XX having symptoms that include bradykinesia and/or proprioceptive  
 XX abnormalities and/or seizures, and in identifying potential modulators  
 XX of motor functions. Cells from the knockout mouse may be used as a  
 XX potential source of differentiated neuronal cells, and for identifying  
 XX agonists and antagonists of neuronal cell growth.  
 XX Sequence: 198 AA;  
 XX  
 Query Match: 91.4%; Score: 870; DB: 22; Length: 198;  
 Best Local Similarity: 91.0%; Pred. No.: 4,66-86;  
 Matches: 162; Conservative: 7; Mismatches: 9; Indels: 0; Gaps: 0;  
 QY 1 MSNVVVSNGSISLERMARGAETIKTSACNRLNLTGVNHEE RDLKHKRDMEEASQPKW 60  
 DB 1 MSNVVVSNGSISLERMARGAETIKTSACNRLNLTGVNHEE RDLKHKRDMEEASQPKW 60  
 QY 61 NPEFQNHKPLGKAYEWGVEKSTGAEYEFSEETKACVKAQPELVAVTNGAVTMM 120  
 DB 61 NPEFQNHKPLGKAYEWGVEKSTGAEYEFSEETKACVKAQPELVAVTNGAVTMM 120  
 QY 121 SQANSETHLVQKTHFADNCAHLAQGTGIRKPAIDUSSEQNKRNKRNTEENVSDGS 178  
 DB 121 SQANSETHLVQKTHFADNCAHLAQGTGIRKPAIDUSSEQNKRNKRNTEENVSDGS 178  
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 DB 121 AVANSETHLVQKTHFADNCAHLAQGTGIRKPAIDUSSEQNKRNKRNTEENVSDGS 178  
 RESULT 15  
 AAB48309  
 10 AAB48309 standard; protein; 198 AA.  
 XX  
 XX AAB48309;  
 XX 02 APR 2001 (first entry)  
 XX Human p27 protein.  
 XX  
 XX S phase kinase associated protein; SKP1; SKP2; SKP3 like protein; ZP;  
 XX S phase kinase associated protein; SKP1; SKP2; SKP3 like protein; ZP;  
 XX Bcl-2; tumor; cytosolic.  
 XX



OS Homo sapiens.  
XX  
PN WC200075184-A1.  
XX  
PD 14-DEC-2000.  
XX  
PF 05-JUN-2000; 2000WC-0515449.  
XX  
PR 04-JUN-1999; 9905-0137494.  
XX  
PA (UYVA ) UNIV YALE.  
XX  
PI Zhang H, Tsvetkov LM, Kondo T;  
XX  
DR WPI; 2001-061703/07.  
DR N-PSDB; AAC84621.  
XX  
PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
XX involves altering levels of proteins such as S-phase kinase associated  
XX proteins 1, 2 and cyclin/Cb53 proteins -  
XX  
PS Claim 25; Page 149-150; 162pp; English.  
XX  
CC The invention relates to methods of altering the polypeptide levels in a  
XX cell, using proteins selected from S-phase kinase associated proteins 1  
XX and 2 (SKP1, SKP2), SKP2-like proteins (2F) and CUL-1 (a member of the  
XX cullin/cbc53 family of proteins). The method is useful for altering the  
XX level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Rad of Bel-2  
XX polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
XX detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
XX that modulate interactions between SKP and target proteins are useful for  
XX treating tumours.  
XX  
SQ Sequence 198 AA;  
  
Query Match 91.4%; Score 870; DB 22; Length 198;  
Best Local Similarity 91.0%; Pred. No. 3.6e-86;  
Matches 162; Conservative 7; Mismatches 9; Indels 0, Gaps 0,  
  
QY 1 MSNVVSNCSSELEPMAPCAFYKPKPSACPNLEGGVNHHELTRELEKHPHMEASOKKW 50  
DB 1 MSNVVSNCSSELEPMAPCAFYKPKPSACPNLEGGVNHHELTRELEKHPHMEASOKKW 50  
  
QY 61 NFEFQNHKPLEKRYEWEVEFKGSIFFYYPPPPPPKACVVPADSESQVSGTPOAVPLMG 120  
DB 61 NFEFQNHKPLEKRYEWEVEFKGSIFFYYPPPPPPKACVVPADSESQVSGTPOAVPLMG 120  
  
QY 121 SCANSEDTLVDOKTDTADNAGLAECVIGIPKKPPATHVSSPPKPKANPTFEENVSDGS 178  
DB 121 SCANSEDTLVDOKTDTADNAGLAECVIGIPKKPPATHVSSPPKPKANPTFEENVSDGS 178

Search completed: May 30, 2003, 08:58:26  
Job time : 39.0956 secs



GenScore version 5.1.6  
Copyright (c) 1993-2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run: 06 May 06 2003 08:55:37 Search time: 33.3385 seconds  
(without alignments)  
392.644 million cell updates/sec

Title: US-09-865-018b-6  
Perfect score: 952  
Sequence: 1 MSNVRVNSGSPSLERMIARQ

Scoring table: BIOSUM62  
Gapop 10 0 0 Gapext 0 5

Searched: 262574 seqs, 2642022 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2600000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptdata/1/1aa/5A\_01MK.pep.\*  
2: /cgn2\_6/ptdata/1/1aa/5B\_01MK.pep.\*  
3: /cgn2\_6/ptdata/1/1aa/6A\_01MK.pep.\*  
4: /cgn2\_6/ptdata/1/1aa/6B\_01MK.pep.\*  
5: /cgn2\_6/ptdata/1/1aa/6C\_01MK.pep.\*  
6: /cgn2\_6/ptdata/1/1aa/6D\_01MK.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	952	100.0	178	4	US-08-794-002-6
2	952	100.0	178	4	US-08-854-039B-6
3	952	100.0	198	1	US-08-275-983B-1
4	952	100.0	198	4	US-08-794-002-22
5	870	91.4	198	1	US-08-406-248-4
6	870	91.4	198	4	US-08-897-333A-2
7	870	91.4	198	4	US-08-240-900B-6
8	870	91.4	198	4	US-08-794-002-2
9	870	91.4	198	4	US-09-457-568-26
10	870	91.4	198	4	US-09-457-646-26
11	865	90.9	391	1	US-08-589-981-2
12	865	90.9	391	4	US-08-457-568-4
13	865	90.9	391	4	US-09-457-646-4
14	865	90.9	198	1	US-08-275-983B-3
15	864	90.7	198	4	US-08-854-039B-2
16	860	90.4	465	4	US-09-457-568-10
17	860	90.4	465	4	US-08-457-646-10
18	860	90.3	380	4	US-09-457-568-8
19	860	90.3	460	4	US-08-457-646-8
20	855	89.8	197	1	US-08-275-983B-2
21	855	89.8	197	4	US-08-240-900B-8
22	855	89.8	197	4	US-09-215-221-57
23	855	89.8	197	4	US-08-794-002-4
24	854	89.6	365	4	US-08-457-568-6
25	854	89.6	465	4	US-09-457-646-6
26	850	89.3	197	3	US-08-415-655-6
27	846	88.9	197	4	US-08-854-039B-4

28	824.5	85.6	195	4	US-09-215-221-54	Sequence 54, Appl
29	820	86.1	212	4	US-09-215-221-49	Sequence 49, Appl
30	811	85.2	177	4	US-09-457-568-12	Sequence 12, Appl
31	811	85.2	177	4	US-09-457-568-12	Sequence 12, Appl
32	811	85.2	334	4	US-09-457-568-16	Sequence 16, Appl
33	811	85.2	334	4	US-09-457-568-16	Sequence 16, Appl
34	811	85.2	348	4	US-09-457-568-14	Sequence 14, Appl
35	811	85.2	348	4	US-09-457-568-14	Sequence 14, Appl
36	809	85.0	194	4	US-09-215-221-52	Sequence 52, Appl
37	808	84.9	193	4	US-09-215-221-53	Sequence 53, Appl
38	805	84.6	194	4	US-09-215-221-51	Sequence 51, Appl
39	762	80.0	180	4	US-09-215-221-55	Sequence 55, Appl
40	758	79.6	180	4	US-09-215-221-50	Sequence 50, Appl
41	549	67.2	145	4	US-09-215-221-56	Sequence 56, Appl
42	390.5	41.0	237	4	US-09-457-568-20	Sequence 20, Appl
43	348.5	41.0	237	4	US-09-457-646-20	Sequence 20, Appl
44	487	40.7	323	4	US-09-457-646-30	Sequence 30, Appl
45	386	40.5	252	4	US-09-457-568-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1  
US-08-794-002-6  
Sequence 6, Application US/08794002  
Patent No. 6316208  
GENERAL INFORMATION:  
APPLICANT: Roberts, James M.  
TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHODS FOR ITS PRODUCTION AND USE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794,002  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/KEYWORD NUMBER: MIV-079.03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 amino acids  
TYPE: amino acid  
Topology: Linear  
MOLECULE TYPE: protein  
US 08-794-002-6

Query Match 100.0%; Score 952; DB 4; Length 178;  
Best Local Similarity 100.0%; Pred No 1.2e-95;  
Matches 178, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY	1	MSNVRVNSGSPSLERMIARQAEYKPSACNLPVNHHELTDLKHKHRDMEASQKWK	60
DB	1	MSNVRVNSGSPSLERMIARQAEYKPSACKNLFVGNHHELTDLKHKHRDMEASQKWK	60
UY	61	NFUPNHHKPLGKYEWEVEKSLPBFYFRPPPPKAKVKVPAQESQDVSGTQAVPLMG	120



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; ZIP: 02109-2170
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Patent in Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/09/794,002
;
; FILING DATE: 03-FEB-1997
;
; CLASSIFICATION: 435
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Vincent, Matthew P
;
; REGISTRATION NUMBER: 36,709
;
; REFERENCE/DOCKET NUMBER: MIV-079 03
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 617-832-1000
;
; TELEFAX: 617-832-7000
;
; INFORMATION FOR SEQ ID NO: 22:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 198 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS:
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; US-08-794-002-22
;
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; Query Match 100.0%; Score 952; DB 4; Length 198;
; Best Local Similarity 100.0%; Pred. No. 1 4e-95;
; Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFGPVNHEELTRDLEKRRDMEASQKRW 60
; Db 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFGPVNHEELTRDLEKRRDMEASQKRW 60
;
; QY 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTROAVPLMG 120
; Db 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTROAVPLMG 120
;
; QY 121 SQANSEDLHLVDQKTDADNOAGLAEOCTGIRKRPATDSSPONKRRANTEENVS DGS 178
; Db 121 SQANSEDLHLVDQKTDADNOAGLAEOCTGIRKRPATDSSPONKRRANTEENVS DGS 178
;
; RESULT 5
;
; US-08-406-248-4
;
; Sequence 4, Application US/08/406248
;
; Patent No. 5736318
;
; GENERAL INFORMATION:
;
; APPLICANT: Munger, Karl
;
; APPLICANT: Jones, D. Leanne
;
; TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
;
; TITLE OF INVENTION: TRANSFORMED CELLS
;
; NUMBER OF SEQUENCES: 6
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusner
;
; STREET: 200 State Street
;
; CITY: Boston
;
; STATE: MA
;
; COUNTRY: USA
;
; ZIP: 02109
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Patent in Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/406,248
;
; FILING DATE:
;
; CLASSIFICATION: 436
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: McDaniel, Patricia A.
;
; REGISTRATION NUMBER: 33,194
;
; REFERENCE/DOCKET NUMBER: HAZ-011
```

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; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 617-330-1300
;
; TELEFAX: 617-330-1311
;
; INFORMATION FOR SEQ ID NO: 4:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 198 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; US-08-406-248-4
;
;
; Query Match 91.4%; Score 870; DB 1; Length 198;
; Best Local Similarity 91.0%; Pred. No. 1 1e-86;
; Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
;
; QY 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFGPVNHEELTRDLEKRRDMEASQKRW 60
; Db 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFGPVNHEELTRDLEKRRDMEASQKRW 60
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; QY 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTROAVPLMG 120
; Db 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTROAVPLMG 120
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; QY 121 SQANSEDLHLVDQKTDADNOAGLAEOCTGIRKRPATDSSPONKRRANTEENVS DGS 178
; Db 121 SQANSEDLHLVDQKTDADNOAGLAEOCTGIRKRPATDSSPONKRRANTEENVS DGS 178
;
; RESULT 6
;
; US-08-897-333A-2
;
; Sequence 2, Application US/08897333A
;
; Patent No. 6177272
;
; GENERAL INFORMATION:
;
; APPLICANT: Nabel, Gary J
;
; APPLICANT: Nabel, Elizabeth G.
;
; TITLE OF INVENTION: METHOD FOR TREATING VASCULAR PROLIFERATIVE DISEASES
;
; TITLE OF INVENTION: WITH p27 AND FUSIONS THEREOF
;
; FILE REFERENCE: 8642/4
;
; CURRENT APPLICATION NUMBER: US/08/897,333A
;
; CURRENT FILING DATE: 1998-07-21
;
; NUMBER OF SEQ ID NOS: 9
;
; SOFTWARE: Patent in Ver. 2.0
;
; SEQ ID NO 2
;
; LENGTH: 198
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
; US-08-897-333A-2
;
;
; Query Match 91.4%; Score 870; DB 4; Length 198;
; Best Local Similarity 91.0%; Pred. No. 1 1e-86;
; Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
;
; QY 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFGPVNHEELTRDLEKRRDMEASQKRW 60
; Db 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFGPVNHEELTRDLEKRRDMEASQKRW 60
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; QY 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTROAVPLMG 120
; Db 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTROAVPLMG 120
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; QY 121 SQANSEDLHLVDQKTDADNOAGLAEOCTGIRKRPATDSSPONKRRANTEENVS DGS 178
; Db 121 SQANSEDLHLVDQKTDADNOAGLAEOCTGIRKRPATDSSPONKRRANTEENVS DGS 178
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; RESULT 7
;
; US-09-240-906-6
;
; Sequence 6, Application US/09240906
;
; Patent No. 6245965
;
; GENERAL INFORMATION:
;
; APPLICANT: ROUSSEL, MARTINE F.
;
; APPLICANT: SNEYNE, RICHARD
;
; APPLICANT: ZINDY, FREDERIQUE
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EARLIER APPLICATION NUMBER: 60/163,682  
EARLIER FILING DATE: 1999-11-05  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 26  
LENGTH: 198  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-457-646-26

Query Match 91.4%; Score 870; DB 4; Length 198;  
Best Local Similarity 91.0%; Pred. No. 1.1e-86;  
Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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QY 61 NEDFQNHKPLECKYEWQVEKGSLSPEFYRPPPKGACKVPAQESQVSTQAVPLMG 120  
DB 61 NEDFQNHKPLECKYEWQVEKGSLSPEFYRPPPKGACKVPAQESQVSTQAVPLMG 120  
QY 121 SOANSEDTLHVQKTDIALNQAGLAECQCTGIPKRPATDDSSPKNKPRANTEENVS DGS 178  
DB 121 PANSSEDTLHVQKTDPSQSGTGLAEQACAGIKRPATDDSSQNKPRANTEENVS DGS 178

RESULT 11  
US-08-589-981-2  
Sequence 2, Application US/08589981  
Patent No. 5672508  
GENERAL INFORMATION:  
APPLICANT: Gyuris, Jeno  
APPLICANT: Lamphere, Lou  
APPLICANT: Beach, David H.  
TITLE OF INVENTION: Inhibitors of Cell-Cycle Progression,  
TITLE OF INVENTION: and Uses Related Thereto  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & CACKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/589,981  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: M11-069  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 391 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-589-981-2

Query Match 90.9%; Score 865; DB 1; Length 391;  
Best Local Similarity 91.0%; Pred. No. 9.7e-86;  
Matches 161; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 SNRVVNSGSPSLERMDARQAEYKPKPSACPNLFPGVNHEELTPDLEKHRRDMEASQKWN 61  
DB 8 SNRVVNSGSPSLERMDARQAEHHPKPSACPNLFPGVDHEELTPDLEKHRRDMEASQKWN 67  
QY 62 FDFQNHKPLECKYEWQVEKGSLSPEFYRPPPKGACKVPAQESQVSTQAVPLMG 121  
DB 68 FDFQNHKPLECKYEWQVEKGSLSPEFYRPPPKGACKVPAQESQVSTQAVPLMG 127  
QY 122 QANSEDTLHVQKTDIALNQAGLAECQCTGIPKRPATDDSSPKNKPRANTEENVS DGS 178  
DB 128 PANSSEDTLHVQKTDPSQSGTGLAEQACAGIKRPATDDSSQNKPRANTEENVS DGS 184

## RESULT 12

US-09-457-568-4  
Sequence 4, Application US/09457568  
Patent No. 6413943  
GENERAL INFORMATION:  
APPLICANT: McArthur, James G  
APPLICANT: Gyuris, Jeno  
APPLICANT: Finer, Mitchell H.  
TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of  
TITLE OF INVENTION: Smooth Muscle Cells  
FILE REFERENCE: 106482.691  
CURRENT APPLICATION NUMBER: US/09/457,568  
EARLIER FILING DATE: 1999-12-09  
EARLIER APPLICATION NUMBER: 60/122,974  
EARLIER FILING DATE: 1999-03-01  
EARLIER APPLICATION NUMBER: 60/163,682  
EARLIER FILING DATE: 1999-11-05  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 391  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-457-568-4

Query Match 90.9%; Score 865; DB 4; Length 391;  
Best Local Similarity 91.0%; Pred. No. 9.7e-86;  
Matches 161; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 SNRVVNSGSPSLERMDARQAEYKPKPSACPNLFPGVNHEELTPDLEKHRRDMEASQKWN 61  
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QY 62 FDFQNHKPLECKYEWQVEKGSLSPEFYRPPPKGACKVPAQESQVSTQAVPLMG 121  
DB 68 FDFQNHKPLECKYEWQVEKGSLSPEFYRPPPKGACKVPAQESQVSTQAVPLMG 127  
QY 122 QANSEDTLHVQKTDIALNQAGLAECQCTGIPKRPATDDSSPKNKPRANTEENVS DGS 178  
DB 128 PANSSEDTLHVQKTDPSQSGTGLAEQACAGIKRPATDDSSQNKPRANTEENVS DGS 184

## RESULT 13

US-09-457-646-4  
Sequence 4, Application US/09457646  
Patent No. 6420345  
GENERAL INFORMATION:  
APPLICANT: Patel, Salil D  
APPLICANT: McArthur, James G  
APPLICANT: Gyuris, Jeno  
TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of  
TITLE OF INVENTION: Smooth Muscle Cells  
FILE REFERENCE: 106482.287  
CURRENT APPLICATION NUMBER: US/09/457,646  
CURRENT FILING DATE: 1999-12-09  
EARLIER APPLICATION NUMBER: 60/122,974  
EARLIER FILING DATE: 1999-03-01  
EARLIER APPLICATION NUMBER: 60/163,682  
EARLIER FILING DATE: 1999-11-05  
NUMBER OF SEQ ID NOS: 32





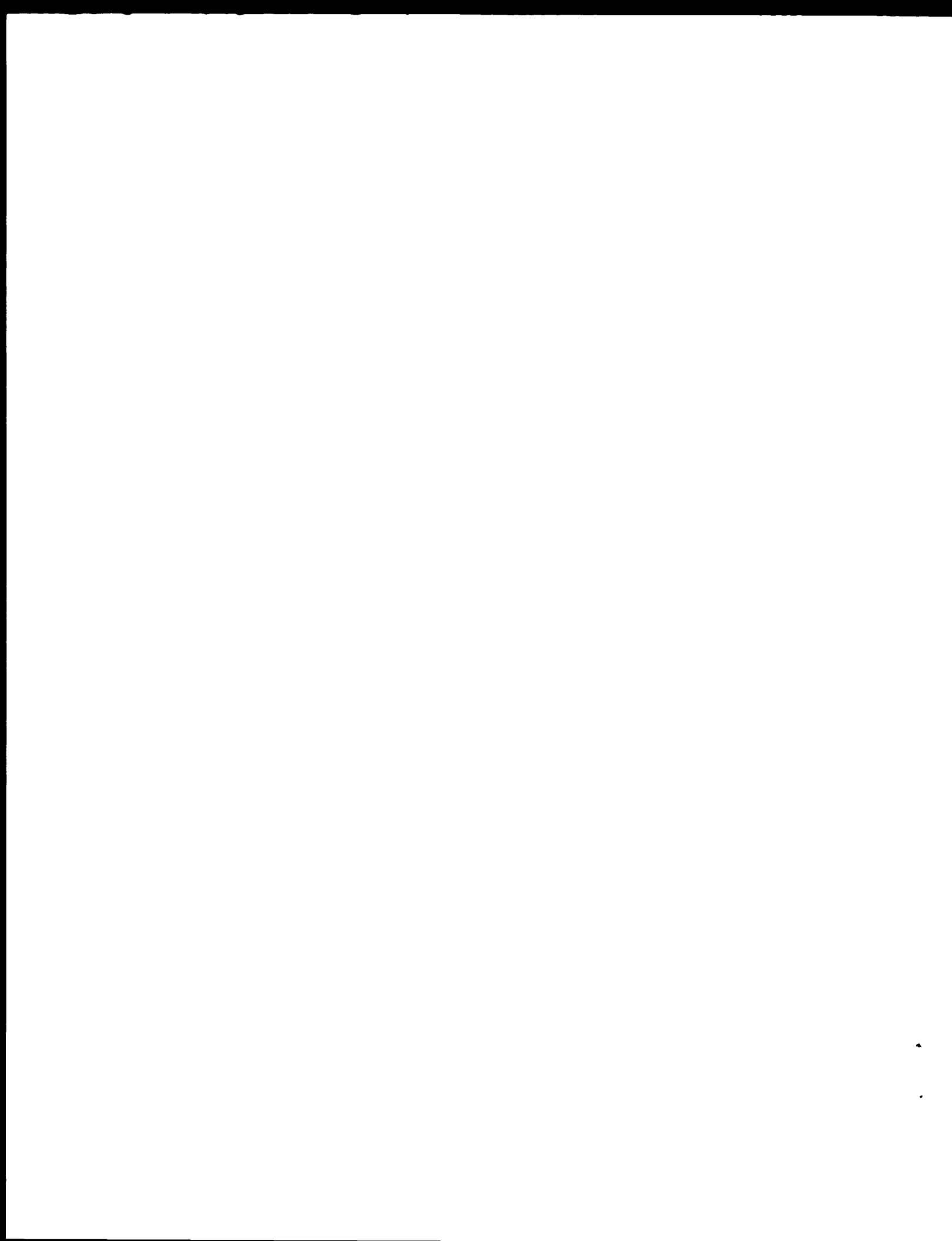
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us-09-865-018b-6.rai

Page 7

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Job time : 13.3385 secs

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OM protein - protein search, using sw model

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991 716 Million cell updates/sec

Title: US-09-865-018b-6  
Perfect score: 952  
Sequence: 1 MSNVRVSGNSSTPRMIAPO DSSPKNPANKPTENVSDGS 178

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Gapop 10.0 : Gapext 0.5

Search-J: 583519 seqs, 16122694 residues  
Total number of hits satisfying chosen parameters: 322519

Minimum DB Seq length: 6  
Maximum DB Seq length: 260000000

Post-processing: Minimum Match: 6%  
Maximum Match: 100%  
Listing first 45 summaries

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- 2: /cqn2-6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep:\*
- 3: /cqn2-6/ptodata/1/pubpaa/US06\_NEW\_PUB pep:\*
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- 14: /cqn2-6/ptodata/1/pubpaa/US60\_PUBCOMB pep:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	872	91.4	198	8	US-09-902-572-2 Sequence 2, Appl
3	865	90.9	391	8	US-08-902-572-2 Sequence 2, Appl
4	863	90.7	199	10	US-09-865-018b-2 Sequence 2, Appl
5	860	90.3	365	8	US-08-902-572-8 Sequence 8, Appl
6	860	90.3	380	8	US-08-902-572-b Sequence 6, Appl
7	846	88.9	197	10	US-09-865-018b-4 Sequence 4, Appl
8	811	85.2	167	8	US-08-902-572-18 Sequence 18, Appl
9	811	85.2	344	8	US-08-902-572-22 Sequence 22, Appl
10	811	85.2	348	8	US-08-902-572-24 Sequence 24, Appl
11	390.5	41.0	237	8	US-08-902-572-26 Sequence 26, Appl
12	386	40.5	252	8	US-08-902-572-28 Sequence 28, Appl
13	377	39.6	76	8	US-08-902-572-29 Sequence 20, Appl
14	167.5	17.6	247	10	US-09-945-297-779 Sequence 770, App
15	163	17.1	164	9	US-09-221-268-5 Sequence 4, Appl
16	163	17.1	164	9	US-09-221-268-5 Sequence 5, Appl
17	163	17.1	164	10	US-09-865-018b-24 Sequence 24, Appl
18	163	17.1	164	10	US-09-940-766-2 Sequence 2, Appl
19	100	10.6	191	10	US-09-744-507-2 Sequence 2, Appl

Sequence 10, Appl  
Sequence 12, Appl  
Sequence 26b, App  
Sequence 15, Appl  
Sequence 159, App  
Sequence 15, Appl  
Sequence 14, Appl  
Sequence 470, App  
Sequence 16, Appl  
Sequence 36182, A  
Sequence 527, App  
Sequence 14, Appl  
Sequence 61, Appl  
Sequence 1, Appl  
Sequence 62, Appl  
Sequence 2, Appl  
Sequence 60, Appl  
Sequence 12955, A  
Sequence 8, Appl  
Sequence 158, App  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 8, Appl  
Sequence 212, App  
Sequence 198, App

#### ALIGNMENTS

##### RESULT 1

US-09-865-018b-6  
Sequence 6, Application US/09865018  
Patent No. US20020110986A1  
GENERAL INFORMATION:

APPLICANT: Massague, Joan  
Roberts, James M.  
Koff, Andrew

POLYAK, Kornelia

TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS PRODUCTION AND USE

NUMREP OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: POLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER: US/09/865,018

FILING DATE: 24-May 2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,039

FILING DATE: 09-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV-079, 04

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 178 amino acids

TYPE: amino acid

TOPOLOGY: linear



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;
; FILING DATE: 24 MAY 2001
; PRIOR APPLICATION DATA: US/08/854,039
; APPLICATION NUMBER: US/08/854,039
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE DESCRIPTION:
; SPOTEN/F CHAPACTERISTICS.
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-865-018b-6
Query Match
Best Local Similarity 90.4%; Score 863; DB 10; Length 198;
Matches 161; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
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Db 1 MSNVRVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPLDLEKHPDMEASQKWN 60
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Db 61 NFDGNHKKPLECKYEWQVEKGSLEPEFYYPYPPPPKPKGACKVPAQESQVSTKQAVPLMG 120
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Db 121 SCANSEDLHLVDQKTDITADNAGLAECQCTGIRKPPATDDSSPQNKRRANRTEENVSDGS 178
QY 121 AVANSEDLHLVDQKTDITADNAGLAECQCTGIRKPPATDDSSPQNKRRANRTEENVSDGS 178
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RESULT 5
US-08-902-572-8
; Sequence 8, Application US/08902572
; Patent No. US20020068706A1
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jenö
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-902-572-6
Query Match
Best Local Similarity 90.4%; Score 860; DB 8; Length 360;
Matches 160; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
QY 2 SNVPSVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPLDLEKHPDMEASQKWN 61
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QY 184 SNVPSVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPLDLEKHPDMEASQKWN 243
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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-902-572-8
Query Match
Best Local Similarity 90.3%; Score 860; DB 8; Length 365;
Matches 160; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
QY 2 SNVPSVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPLDLEKHPDMEASQKWN 61
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QY 62 FDFQNHKKPLECKYEWQVEKGSLEPEFYYPYPPPPKPKGACKVPAQESQVSTKQAVPLMG 121
Db 229 FDFQNHKKPLECKYEWQVEKGSLEPEFYYPYPPPPKPKGACKVPAQESQVSTKQAVPLMG 121
QY 122 QANSEDLHLVDQKTDITADNAGLAECQCTGIRKPPATDDSSPQNKRRANRTEENVSDGS 178
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RESULT 6
US-08-902-572-6
; Sequence 6, Application US/08902572
; Patent No. US20020068706A1
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jenö
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-902-572-6
Query Match
Best Local Similarity 90.4%; Score 860; DB 8; Length 360;
Matches 160; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
QY 2 SNVPSVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPLDLEKHPDMEASQKWN 61
Db 184 SNVPSVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPLDLEKHPDMEASQKWN 243
; SEQUENCE CHARACTERISTICS:
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; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/902,572
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069,03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-7000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 22
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-902-572-22

Query Match 85.2%; Score 811; DB 8; Length 334;
Best Local Similarity 90.4%; Pred. No. 5, 1e-69;
Matches 150; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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RESULT 10
US-08-902-572-24
; Sequence 24, Application US/08/902,572
; Patent No. US2002008706A1
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069,03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-7000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 26
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-902-572-24

Query Match 85.2%; Score 811; DB 8; Length 348;
Best Local Similarity 90.4%; Pred. No. 5, 3e-69;
Matches 150; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 12 SLEPMACACAEYKPKSACPNLFGPVNHEELTPDLKHKRPDMEEASORKNWFDFONHKPLE 71
DB 12 SLEPMACACAEYKPKSACPNLFGPVNHEELTPDLKHKRPDMEEASORKNWFDFONHKPLE 71
QY 72 GKYVQVEKGSLSPEFYRPPPPKGAQKVAQESQVSVTPQAVPLMGSQANSEDLHLV 131
DB 72 GKYVQVEKGSLSPEFYRPPPPKGAQKVAQESQVSVTPQAVPLMGSQANSEDLHLV 131
QY 132 DQKIDADNAGIAEQCTGIRKRPATDSSPQNKPRNTEENVSDG 177
DB 132 DPKTDPDSQTGLAEQAGIEKRPATDSSSTQNKPRNTEENVSDG 177

RESULT 11
US-08-902-572-26
; Sequence 26, Application US/08/902,572
; Patent No. US2002008706A1
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069,03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-7000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 26
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-902-572-26
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GenInfo version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 08:54:42 : search time 14.94s seconds  
(without alignments)  
1144.739 Million cell updates/sec

Title: US-09-865-018b-6  
Perfect score: 952  
Sequence: 1 MSNVRVSNCSPLERMDAPQ.....PESPNKFRANPTTEENVSDGS 178

Scoring table: BLOSUM62  
Gapop 10 0 , Gapext 0.5

Searched: 283224 seqs, 9614422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR73.  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. Val. is the number of hits predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	860	40.3	194	2 152718	gene p27kip1 prote
2	855	39.8	197	2 149064	cyclin-cdk inhibit
3	197	23.7	210	2 151683	cyclin-dependent k
4	194.5	20.6	216	2 G03424	cyclin-dependent k
5	191	23.1	348	2 149262	cyclin-cdk inhibit
6	187	19.6	164	2 184725	tumor suppressor p
7	168.5	17.7	159	2 149323	tumor suppressor p
8	165.5	17.4	143	2 A49438	p53 tumor suppress
9	163.5	17.2	181	2 168674	cyclin-dependent k
10	161.5	17.0	181	2 154380	cyclin-dependent k
11	136.5	14.3	258	2 124499	hypothetical prote
12	113	11.9	184	2 124496	hypothetical prote
13	100	10.5	191	2 T01132	cyclin-dependent k
14	93	9.8	246	1 S49770	hypothetical prote
15	89.5	9.4	487	2 G85272	hypothetical prote
16	87	9.1	209	2 C08850	conserved hypotet
17	86	9.0	914	2 140529	penicillin-binding
18	85.5	9.0	937	2 A56517	nucleoporin Nup98
19	84.5	8.9	246	2 S57075	hypothetical prote
20	84.5	8.9	369	2 B43715	protein M homolog
21	84.5	8.9	894	2 S25332	RRN6 protein - yea
22	84.5	8.9	1004	2 H88562	protein C07A9.3 [i
23	84.5	8.9	1044	2 S40704	hypothetical prote
24	84	8.8	404	2 H84648	hypothetical prote
25	84	8.8	754	2 A56619	female sterile hom
26	84	8.8	1992	1 S02771	myosin heavy chain
27	83.5	8.8	735	2 S54147	alpha adducin - ra
28	83.5	8.8	1014	2 S32613	HEX2 protein - yea
29	83	8.7	2448	2 T00249	cell proliferation

30	82.5	8.7	834	2 T42702	hypothetical prote
31	82.5	8.7	858	2 S15762	neurofilament trip
32	82	8.6	272	2 A24824	tropocollin T, fast s
33	82	8.6	444	2 A40860	prolactin protein k
34	82	8.6	508	2 T02684	MYB-related transcr
35	82	8.6	897	2 T21688	hypothetical prote
36	82	8.6	1045	2 T18373	erythrocyte bindin
37	81.5	8.6	246	2 T12760	probable lipoprote
38	81.5	8.6	1011	2 T13055	dynamitin associated
39	81.5	8.6	1057	2 H83273	dynamitin associated
40	81.5	8.6	1094	2 T13053	dynamitin associated
41	81.5	8.6	1097	2 T13504	hypothetical prote
42	81.5	8.6	1102	2 T39943	hypothetical prote
43	81.5	8.6	1211	2 T42230	AF4 protein - mous
44	81.5	8.6	1944	2 A59438	KIAA1424 protein l
45	81	8.5	383	2 G86197	hypothetical prote

ALIGNMENTS

RESULT 1

152718  
gene p27kip1 protein - human  
C:Species: Homo sapiens (man)  
C>Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000  
C:Accession: 152718  
P:Pieterpol, J.A.; Bohlander, S.K.; Sato, Y.; Papadopoulos, N.; Liu, B.; Friedman, C.  
Cancer Res. 55, 1206-1210, 1995  
A:Title: Assignment of the human p27Kip1 gene to 12p13 and its analysis in leukemias.  
A:Reference number: 152718, MUID:95188144, PMID:7882309  
A:Accession: 152718  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-198 <RES>  
A:Cross-references: CR 576588, NID:9508402, PUBN:AAU14244 1, PDB:1J4261944  
C:Genetics:  
A:Gene: p27Kip1  
A:Introns: 159/1

Query Match 90.3% Score 860; DB 2; Length 198;  
Best Local Similarity 89.9% Pred. No. 5/e-67;  
Matches 160, Conservative 8, Mismatches 10, Indels 0, Gaps 0,

Cy	1	MSNVPSVNSGFS:EPMDAPQAFYKTSACPNIEGPNVNHETLSTLEKHPDMEASQPKW 60	
ib	1	MSNVPSVNS:SPSLPMLAPQADHPKPSA:FNLE:PVGHPFLTRLEKHPDMEASQPKW 60	
Cy	61	NEFQNHKFLPGKYEW:FEVKESLI:FEYYSFG:KPKACAKVPA:KSNQVSL:KAVLW: 120	
ib	61	NEFQNHKFLPGKYEW:FEVKESLI:FEYYSFG:KPKACAKVPA:KSNQVSL:KAVLW: 120	
Cy	121	SDANSETHLVTKTTTADNQAGLAEOCTGTRKPPATDSSPNKFRANPTTEENVSDGS 178	
ib	121	AFANSETHLVDPKTPFSDSGTGLAEEACGIPKFPATDSSGNKFRANPTTEENVSDGS 178	

RESULT 2

149064  
cyclin-cdk inhibitor p27 - mouse  
N:A:Alternate names: Cdi p27, Gl cyclin-cyclin-dependent kinase inhibitor p27  
C:Species: Mus musculus (house mouse)  
C>Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 05-Nov-1999  
C:Accession: 149064  
R:Toyoshima, H.; Hunter, T.  
Cell 78, 67-74, 1994  
A:Title: p27, a novel inhibitor of Gl cyclin-Cdk protein kinase activity, is related  
A:Reference number: A54839; MUID:94306519; PMID:8033213  
A:Accession: 149064  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-197 <RES>  
A:Cross-references: EMBL 352773, PUBN:AAU11449 1, PDB:352772



C:Genetics:  
A:Gene: WAF1

Query Match 19.6%; Score 187; DB 2; Length 164;

Best Local Similarity 25.9%; Pred. No. 4 to 39;

Matches 42; Conservative 25; Mismatches 65; Indels 25; Gaps 4;

QY 17 DAPAEYPPKPSACRNLFQVNHHEELFMLEKHPFMEASQPKWNFFQNHKPLEGKYEW 75

DB 6 DVPPVPH-RSKVCPFLFPVNSEQLSPDCDALMASCLOEAPERNWPFATETPLEGNYVW 64

QY 77 QVEKGSILPEFYPPPPPKKAKVPAQESQVDSGTRQAVPLMGSOANSEDTHLVDOKTD 136

DB 65 EVRSPGLPKVYLSL-----GSKRRDDLGSGKPPSTSSALLQGP 105

QY 137 TADNAGLAEOCTGIRKRPATDDSSP-----QNKPRNPT 170

DB 106 APEDHVALSLSCTLVSHAPERPEPSGGTSGGRKRPQT 145

# RESULT 7

I49023

tumor suppressor p21 WAF1/CIP1 [imported] - mouse

C:Species: Mus musculus (house mouse)

C>Date: 92-Jul-1992 #sequence\_revision 92 Jul-1992 #text\_change 20-Jun-2000

C:Accession: I49023; I49296

E:Baiffr, K., Sawasaki, L., Boskin, J., Miki, J., P. Chodid, M., Reed, S., Mock, B., Giv

Oncogene 9, 3017-3020, 1994

A:Title: Molecular cloning, sequencing, chromosomal localization and expression of mouse

A:Reference number: I49023, MIM: 646875; FIM: 804687

A:Accession: I49023

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 155 SRS

A:Cross-references: EMBL:009507; NID:0595302; PIR:AA06456; PIR:0595302

R:El-deiry, W.S.; Tokino, T.; Velculescu, V.; Lin, J.D.; Burrell, M.; Hill

Cancer Res. 55, 2910-2919, 1995

A:Title: Topological control of p21WAF1/CIP1 expression in normal and neoplastic tissues

A:Reference number: I49296, MIM: 6531858; FIM: 7736423

A:Accession: I49296

A>Status: nucleic acid sequence not shown, translation not shown, translated from GB/EM

A:Molecule type: mRNA

A:Residues: 155 SRS

A:Cross-references: EMBL:04417; NID:04417; PIR:AA05223; PIR:04417

C:Genetics:

A:Gene: Waf1

Query Match 17.7%; Score 168.5; DB 2; Length 159;

Best Local Similarity 25.8%; Pred. No. 1.7e-07;

Matches 42; Conservative 25; Mismatches 65; Indels 25; Gaps 4;

QY 17 DAPAEYPPKPSACRNLFQVNHHEELFMLEKHPFMEASQPKWNFFQNHKPLEGKYEW 76

DB 6 DVPPVPH-RSKVCPFLFPVNSEQLSPDCDALMASCLOEAPERNWPFATETPLEGNYVW 64

QY 77 QVEKGSILPEFYPPPPPKKAKVPAQESQVDSGTRQAVPLMGSOANSEDTHLVDOKTD 136

DB 65 EVRSPGLPKVYLSL-----GSKRRDDLGSGKPPSTSSALLQGP 105

QY 137 TADNAGLAEOCTGIRKRPATDDSSP-----QNKPRNPT 170

DB 106 APEDHVALSLSCTLVSHAPERPEPSGGTSGGRKRPQT 145

# RESULT 8

A49438

p53 tumor suppressor mediator WAF1 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 07 Apr 1994 #sequence\_revision 18-Nov-1994 #text\_change 18-Nov-1994

C:Accession: A49438

R:El-deiry, W.S.; Tokino, T.; Velculescu, V.E.; Levy, D.R.; Parsons, P.; Trent, J.M.; Li

Cell 75, 817-825, 1993

A:Title: WAF1, a potential mediator of p53 tumor suppression.

A:Reference number: A49438; MIM: 6406197; FIM: 8242752

A:Accession: A49438

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1143 SLL

A>Note: sequence extracted from NCI backbone (NCIN-140907, NCI-P 140908)

Query Match 17.4%; Score 165.5; DB 2; Length 143;

Best Local Similarity 26.1%; Pred. No. 2.8e-07;

Matches 41; Conservative 27; Mismatches 64; Indels 25; Gaps 4;

QY 17 DAPAEYPPKPSACRNLFQVNHHEELFMLEKHPFMEASQPKWNFFQNHKPLEGKYEW 76

DB 6 DVPPVPH-RSKVCPFLFPVNSEQLSPDCDALMASCLOEAPERNWPFATETPLEGNYVW 64

QY 77 QVEKGSILPEFYPPPPPKKAKVPAQESQVDSGTRQAVPLMGSOANSEDTHLVDOKTD 136

DB 65 EVRSPGLPKVYLSL-----GSKRRDDLGSGKPPSTSSALLQGP 103

QY 137 TADNAGLAEOCTGIRKRPATDDSSP-----QNKPRNPT 170

DB 104 APEDHVALSLSCTLVSERPEDSPGGTSGGRKRPQT 140

# RESULT 9

I68674

cyclin dependent kinase - human (fragment)

N:Alternate names: probable DNA synthesis inhibitor

C:Species: Homo sapiens (man)

C:Title: Human cyclin dependent kinase - human (fragment) - text change 01-Dec 2000

C:Accession: I68674; A49437; I53412; S39357

E:Moynihan, S.; Giv, B.; H.; Lee, P.D.; Malkin, D.; Holl, S.H.; Andrulis, J.L.

Hum Mol Genet 4, 1089-1092, 1995

A:Title: Two variants of the CIP1/WAF1 gene occur together and are associated with hu

A:Reference number: I54480; MIM: 6504154; FIM: 7655454

A:Accession: I68674

A>Status: preliminary, translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1181 SRS

A:Cross-references: GR I47233, NID:0486878, PIR:AA06056; PIR:0486879

R:Baiffr, J.W.; Adams, G.B.; Wei, N.; Keyomarsi, K.; Elledge, S.J.

Cell 75, 805-816, 1993

A:Title: the p21 Cdk-interacting protein Cipl is a potent inhibitor of G1 cyclin-depe

A:Reference number: A49437; MIM: 6456196; FIM: 842751

A:Accession: A49437

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1818 SRS

A:Cross-references: GR I425610; NID:0425142; PIR:AA016109; PIR:0425143

R:Noda, A.; Ning, Y.; Venables, S.F.; Pereira Smith, O.M.; Smith, J.R.

Exp. Cell Res. 211, 90-98, 1994

A:Title: Cloning of senescent cell-derived inhibitors of DNA synthesis using an expe

A:Reference number: I53412, MIM: 64170884; FIM: 8125163

A:Accession: I53412

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1818 SRS

A:Cross-references: GR I426165; NID:0418017; PIR:AA019811; PIR:0433742

R:Xiong, Y.; Han, G.J.; Zhang, H.; Russo, P.; Kobayashi, R.; Beach, D.

Nature 365, 701-704, 1993

A:Title: p21 is a universal inhibitor of cyclin kinases.

A:Reference number: S39357; MIM: 6401455; FIM: 8259214

A:Accession: S39357

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1818 SRS

A:Cross-references: GR S67388, NID:0453334, PIR:AA06046; PIR:0453335

C:Genetics:

A:Gene: CIP1/WAF1

Query Match 17.2%; Score 163.5; DB 2; Length 181;

Best Local Similarity 28.4%; Pred. No. 5.5e-07;

Matches 48; Conservative 24; Mismatches 74; Indels 23; Gaps 5;



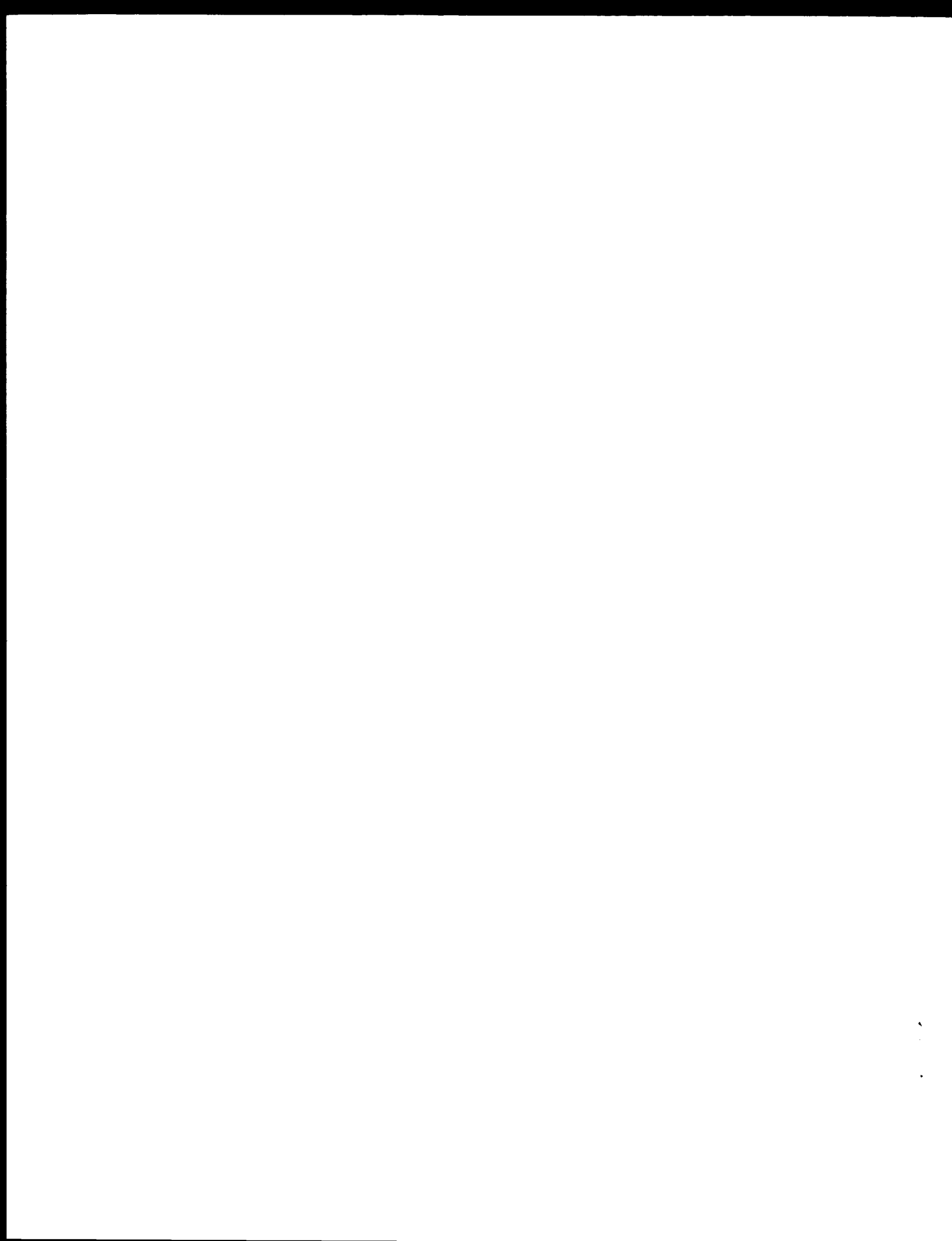
A:Accession: F84624  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-191 <STO>  
A:Cross-references: GR:AF062093; NID:g124.706; PIDN AAC23758.1; GSPR:GN00139  
C:Genetics:  
A:Gene: F26B6.8, At2g23430  
A:Map position: 2  
A:Introns: 55, 5, 21, 2, 13, 2

Query Match 10.5%; Score 100; DB 2; Length 191;  
Best Local Similarity 48.4%; Pred. No. 0.17;  
Matches 15; Conservative 10; Mismatches 6; Indels 0; Gaps 0;  
QY 50 RDMERASORKNFDQFNHKLPGKYEWE 80  
DB 161 KCLKFKKKKYNFDEFEKPLEGKYEWE 191  
PSSM 14  
S49770  
hypothetical protein YDR174w yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein YD9395.07  
C:Species: Saccharomyces cerevisiae  
C:Date: 10-Sep-1999 #supra-division 10-Sep-1999 #text\_change 19-Apr-2002  
C:Accession: S49770  
R:Murphy, L.; Harris, D.E.  
submitted to the EMBL Data Library, November 1994  
A:Reference number: S49764  
A:Accession: S49770  
A:Molecule type: DNA  
A:Residues: 1-246 <MURS>  
A:Cross-references: EMBL:Z46727; NID:g128283; PID:g128280; GSPR:GN00004; MIPS YDR174w  
C:Genetics:  
A:Gene: SGD:HM01; MIPS:YDR174w  
A:Cross-references: SGD:S0002581  
A:Map position: 4R  
C:Superfamily: yeast hypothetical protein YDR174w; HMG box homology  
F:103-185/Domain: HMG box homology <HMG>

Query Match 9.8%; Score 93; DB 1; Length 246;  
Best Local Similarity 19.6%; Pred. No. 0.93;  
Matches 33; Conservative 32; Mismatches 49; Indels 54; Gaps 6;  
QY 15 RMDAGAYPKPSACRNLPGVNHLETRDLEKRRRMEASQKRW----NFDFQNHKPL 70  
DB 125 REDQKAGLP-----PLSSTEITQETSKKMKLSUNEKEKQAYNVELENYQRE 174  
QY 71 EGYEWEKESGLPEFYRPPKPGACKVPAGESODVSGTQAVPLMGSOANSEDTHL 130  
DB 175 KSKY-LEAKKNTLP-----PA--SLNGPTHAPVPIPTSLQHAAE--- 212  
QY 131 VDQKTDATDAGLAEGQCTGIRKRPATDSSSPONKRANRTEENVSDGS 178  
DB 213 -----PPVEKRPFHDDGSSKKKKKKKKKKKK 242

Search completed: May 30, 2003, 09:02:46  
Job time : 16.9483 secs

RESULT 15  
G86272  
hypothetical protein F7A19.5 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001  
C:Accession: G86272  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Conway, A.R.; Cressy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Robinson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.P.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.





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OM protein - protein search, using sw model

Run on: May 30, 2003, 08:52:42 : Search time 7.59015 seconds  
(without alignments)  
972.608 Million cell updates/sec

Title: US-09-865-018B-6

Perfect score: 952

Sequence: 1 MSNVRVNSGSPSIRMDARQ.....DSSPQNKRNKRINVS DGS 178

Scoring table: BLOSUM62

Gapop 10 0 , Gapext 0.5

Searched: 112892 seqs, 41475328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	952	100	0	1	CDNB_MUSVI
2	919	96.5	198	1	CDNB_FELCA
3	870	91.4	198	1	CDNB_HUMAN
4	855	89.8	197	1	CDNB_MOUSE
5	838	88.0	198	1	CDNB_CRIGR
6	196.5	20.6	316	1	CDNC_HUMAN
7	191	20.1	348	1	CDNC_MOUSE
8	168.5	17.7	159	1	CDNL_MOUSE
9	166.5	17.5	164	1	CDNL_FELCA
10	164	17.1	164	1	CDNL_HUMAN
11	89.5	9.4	514	1	WRK3_APATH
12	89	9.3	548	1	KIRP_MOUSE
13	86	9.0	914	1	PBPA_BACSU
14	85.5	9.0	937	1	N198_PAT
15	84.5	8.9	236	1	YJ26_YEAST
16	84.5	8.9	369	1	MX_STRPY
17	84.5	8.9	894	1	RPN2_YEAST
18	84.5	8.9	1231	1	YRT3_CAEEL
19	84	8.8	801	1	BD22_HUMAN
20	84	8.8	1969	1	MYSA_CAFEL
21	84	8.8	2033	1	PVFI_HUMAN
22	83.5	8.8	735	1	AGUA_KAI
23	83.5	8.8	1014	1	HX22_YEAST
24	83	8.7	3473	1	ATFX_HUMAN
25	82.5	8.7	857	1	NFM_CHICK
26	82	8.6	258	1	TRT3_PAT
27	82	8.6	494	1	HR25_YEAST
28	81	8.5	697	1	YF9C_SCHPO
29	80	8.4	1109	1	TCF8_PAT
30	79.5	8.4	1020	1	RER_HUMAN
31	79.5	8.4	1839	1	CYAA_SACKL
32	79	8.3	450	1	INVO_LEMCA
33	79	8.3	475	1	CAPI_HUMAN

34 79 8 3 631 1 XPC1\_MOUSE  
35 79 8 3 2441 1 CRP\_MOUSE  
36 78.5 8 2 937 1 N198\_HUMAN  
37 78.5 8 2 1167 1 Z02\_MOUSE  
38 78.5 8 2 1210 1 AF4\_HUMAN  
39 78.5 8 2 1493 1 M3K1\_MOUSE  
40 78.5 8 2 3149 1 TEGU\_EBV  
41 78 8 2 261 1 XC92\_HAEIN  
42 78 8 2 513 1 WRK3\_ARATH  
43 78 8 2 536 1 ZF94\_PAT  
44 78 8 2 559 1 ENL\_HUMAN  
45 77.5 8 1 561 1 TARA\_MOUSE

Q60596 mus musculus  
P45481 mus musculus  
P52948 homo sapien  
Q92001 mus musculus  
P41825 homo sapien  
P53349 mus musculus  
P03186 epstein-bar  
P44154 haemophilus  
Q92970 arabidopsis  
Q92XK3 rattus norv  
Q03111 homo sapien  
Q99KW3 mus musculus

## ALIGNMENTS

RESULT 1  
CDNB\_MUSVI  
ID CDNB\_MUSVI STANDARD; PRT; 178 AA.  
AC 146524  
DI 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase  
inhibitor p27) (p27Kip1) (Fragment).  
GN CDKN1B.  
OS Mus musculus (American mink).  
OC Eukaryota, Metazoa, Chordata, Claviata, Vertebrata, Euteleostomi;  
OC Mammalia, Eutheria, Carnivora, Fissipedia; Mustelinae;  
OC Mustela.  
CX NCBI\_LaxID=96b7;  
RN [1]  
PP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=94306518; PubMed=9033212;  
RA Polyak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M.,  
Tempst P., Massague J.;  
RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a  
potential mediator of extracellular antimitogenic signals.";  
PL Cell 78:59-66(1994).  
RN [2]  
FP FUNCTION.  
RX MEDLINE=94116862; PubMed=8288131;  
RA Polyak K., Kato J.-Y., Solomon M.J., Sherr C.J., Massague J.,  
Roberts J.M., Koff A.;  
RT "p27Kip1, a cyclin-cdk inhibitor, links transforming growth  
factor-beta and c-myc inhibition to cell cycle arrest";  
PL Genes Dev. 8:922(1994).  
CC -!- FUNCTION: Involved in G1 arrest. May mediate TGF-beta-induced G1  
arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,  
cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin  
NUP50 is required for nuclear import and for degradation of  
phosphorylated p27Kip1 after nuclear import (By similarity).  
CC -!- SUBUNIT: Interacts with NUP50 (By similarity).  
CC -!- CELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.  
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration  
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EMBL: U09466, AAA02341, ..  
InterPro: IPR003175, CDI.  
Pfam: PF02234, CDI; 1.  
KW Cell cycle, Nuclear protein.  
FT DOMAIN 153 169 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)  
FT NON\_TER 178 178  
FT REGION 178 AA: 20129 MW; 104018440-14738 CFC64;  
Sequence: 178 AA: 20129 MW;

















PN SEQUENCE FROM N.A.  
 RP STRAIN: 168 / Matburg;  
 RX MEDLINE: 96149105; PubMed: 8760412;  
 RA Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,  
 RA Serron P.;  
 RT "Sequence analysis of the *Bacillus subtilis* chromosome region between  
 RT the *serA* and *kdg* loci cloned in a yeast artificial chromosome";  
 PL Microbiology 142:2005-2016(1996);  
 RN [13]  
 RP GROWTH REQUIREMENTS.  
 RX STRAIN 168;  
 RX MEDLINE: 98389671; PubMed: 921295;  
 RA Murray T., Popham D.L., Setlow P.;  
 RT "Bacillus subtilis cells lacking penicillin-binding protein 1 require  
 RT increased levels of divalent cations for growth.";  
 RL J. Bacteriol. 180:4555-4563(1998).  
 RN [14]  
 RP SUBCELLULAR LOCATION.  
 RX STRAIN: 168;  
 RX MEDLINE: 99255546; PubMed: 10322023;  
 RA Pedersen L.B., Angert E.R., Setlow P.;  
 RT "Septal localization of penicillin-binding protein 1 in *Bacillus*  
 RT *subtilis*";  
 RL J. Bacteriol. 181:3201-3211(1999).  
 CC [-] FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED  
 CC PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A  
 CC PENICILLIN-INSENSITIVE TRANSGLYCOSYLASE N-TERMINAL DOMAIN  
 CC (FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE  
 CC TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE  
 CC SUBUNITS) (BY SIMILARITY).  
 CC [-] PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.  
 CC [-] SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN, PROBABLY FOUND ALL  
 CC OVER THE WHOLE CELL AT LOW CONCENTRATIONS. ALSO LOCALIZES TO THE  
 CC DIVISION SITE IN VEGETATIVE CELLS.  
 CC [-] DEVELOPMENTAL STAGE: EXPRESSION IS CONSTANT DURING GROWTH,  
 CC DECREASES DURING SPORE FORMATION AND IS INDUCED APPROXIMATELY 15 MIN  
 CC INTO SPORE GERMINATION.  
 CC [-] PTM: THE PRODUCT EXPRESSED FROM THE TRANSLATION OF THE *PONA* GENE  
 CC APPEARS AS TWO BANDS ON A GEL (1A AND 1B), BUT THE SPECIFIC AMINO  
 CC ACID SEQUENCE OF EACH PROTEIN IS UNKNOWN.  
 CC [-] PTM: THE N-TERMINUS IS BLOCKED.  
 CC [-] MISCELLANEOUS: CELLS LACKING THE PROTEIN REQUIRE INCREASED LEVELS  
 CC OF MG2+ OR CA2+ FOR GROWTH AND GERMINATION. APPROXIMATELY 50% OF  
 CC CELLS WITHOUT THE PROTEIN CONTAIN ABNORMAL FTSG RINGS, SUGGESTING  
 CC IT IS INVOLVED IN SEPTUM SYNTHESIS; INCREASED LEVELS OF MG2+ OR  
 CC CA2+ ONLY PARTIALLY ELIMINATE THE SEPTATION DEFECTS.  
 CC [-] SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE  
 CC TRANSGLYCOSYLASE FAMILY.  
 CC [-] SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE  
 CC TRANSPEPTIDASE FAMILY.  
 CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL: 011883; AAC4547.1; -;  
 CC EMBL: L47838; AAB38459.1; -;  
 CC EMBL: 299115; CAB14148.1; -;  
 CC Subtilist; BG10934; PONA.  
 CC InterPro: IPR003461; PNA.F11.  
 CC InterPro: IPR001264; GT\_51.  
 CC InterPro: IPR001460; Transpeptidase.  
 CC Pfam: PF00041; fo3; 1.  
 CC Pfam: PF09905; Transpeptidase; 1.  
 CC Pfam: PF00912; Transglycosyl; 1.  
 CC SMART: SM00060; FN3; 1.  
 CC Peptidolysin synthesis; Cell wall; Translase; Glycosyltransfase.

KW Hydrolase; Multifunctional enzyme; Transmembrane; Signal-anchor;  
 KW Antibiotic resistance; Complete proteome.  
 FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 38 58 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)  
 FT POTENTIAL.  
 FT DOMAIN 59 914 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 77 245 TRANSGLYCOSYLASE.  
 FT DOMAIN 420 662 TRANSPEPTIDASE.  
 FT ACT\_SITE 390 390 ACYLATED BY PENICILLIN (BY SIMILARITY).  
 SQ SEQUENCE 914 AA; 94566 MW; 6474630 Da; 10044; 10044;  
 Query Match 9.0%; Score 86; DB 1; Length 914;  
 Best Local Similarity 22.1%; Freq. No. 12;  
 Matches 48; Conservative 35; Mismatches 88; Indels 46; Gaps 10;  
 QY 6 VSNQSYSLERMDA-RQAEYKPSACRNLFQF-VNHEELTRDLK-----HRRD 51  
 DB 643 VDDGSGSEKPSDWEATVEKGSNPAKLAGPNTPSDKLTVEYFKGTAPSTVSKTYEKEE 702  
 QY 52 MEASQ-----PKWNFD-----FONHKPLEGKYEWQVEKGSLEPFYRYP 91  
 DB 703 KEELAKSLGYNVYKDNQSLTSLSNWYDQATFAVKQSVGG-SYSEIQNSSAKEAVISC 761  
 QY 92 PRFP---KRAKVFQAESEIVSOTPAVPI-----MGSQANSEIHILVQKIDTADNQA 142  
 DB 762 VQPSVYKFEVTAIVSLGKSTASTSYEVKPAEDGELKKLQVQIDCKQDEKTD-DTQT 820  
 QY 143 GLAEOTGIPKPRATDS-SPONKPAKRNTEENVSDGS 178  
 DB 821 DUSQKDGQIDQDQIDLSINDQKQKQDNTNTPSDNN 857  
 RESULT 14  
 NU98\_RAT ID NU98\_RAT STANDARD; PKT; 937 AA.  
 AC P49793;  
 DT 01-OCT-1996 (Ref. 34, Created)  
 DT 01-OCT-1996 (Ref. 34, Last sequence update)  
 DT 15-JUN-2002 (Ref. 41, Last annotation update)  
 DE Nuclear pore complex protein Nup98 (Nucleoporin Nup98) (98 kDa  
 DE nucleoporin).  
 GN NUP98  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia, Scuriognathi, Muridae, Murinae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=95254530; PubMed=7736573;  
 RA Radu A., Moore M.S., Blobel G.;  
 RT "The peptide repeat domain of nucleoporin Nup98 functions as a  
 RT docking site in transport across the nuclear pore complex.";  
 RL Cell 81:215-222(1995).  
 CC [-] FUNCTION: PLAYS A ROLE IN THE BIDIRECTIONAL TRANSPORT ACROSS THE  
 CC NUCLEOPORIN COMPLEX (NPC). THE REPEAT DOMAIN HAS A DIRECT ROLE IN  
 CC THE TRANSPORT.  
 CC [-] SUBCELLULAR LOCATION: Nuclear pore complex  
 CC [-] DOMAIN: CONTAINS G-L-F-G REPEATS.  
 CC [-] PTM: THE N-TERMINUS IS BLOCKED.  
 CC [-] SIMILARITY: BELONGS TO THE GLEF FAMILY OF NUCLEOPORINS.  
 CC  
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 CC  
 CC EMBL: L39991; AAC42054.1; -;  
 CC InterPro: IPR004325; Nucleoporin\_FG  
 CC Pfam: PF09905; Nucleoporin\_F3; 46.



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OM protein - protein search, using sw model

Run on: May 30, 2003, 08:53:57 Search time: 31.3466 seconds  
(without alignments)  
1181.337 Million cell updates/sec

Title: US-09-865-018b-6

Perfect score: 952

Sequence: 1 MSNVRVNSGSPSLERMDARQ ... DSSPQNKANKTEFNVSUQS 178

Scoring table: BLOSUM62

Gapop 10 0, Gapext 0.5

Searched: 671580 seqs, 20604715 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_minc.\*
- 8: sp\_organell.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	910	95.6	198	6 Q9BDC3	Q9BDC3 sus scrofa
2	864	90.8	198	4 Q9NYG6	Q9NYG6 homo sapien
3	864	90.7	199	4 Q9HUS*	Q9HUS* homo sapien
4	860	90.3	198	4 Q96TE0	Q96TE0 homo sapien
5	840	88.2	197	11 Q08769	Q08769 rattus norv
6	835	87.7	197	11 Q35792	Q35792 rattus norv
7	791	83.1	172	6 Q9EAS5	Q9EAS5 sus scrofa
8	769	80.8	158	4 Q43806	Q43806 homo sapien
9	333	35.0	179	13 Q90YX4	Q90YX4 brachydanio
10	197	20.7	210	13 Q91703	Q91703 xenopus lac
11	193	20.3	209	13 Q91646	Q91646 xenopus lac
12	191.5	20.1	335	11 Q41806	Q41806 mus musculu
13	187	19.6	164	11 Q64315	Q64315 rattus norv
14	168	17.6	42	4 Q9UH60	Q9UH60 homo sapien
15	167.5	17.6	164	4 Q96LE1	Q96LE1 homo sapien
16	161.5	17.6	181	4 Q14010	Q14010 homo sapien

#### ALIGNMENTS

##### RESULT 1

Q9BDC3 ID Q9BDC3 PRELIMINARY; PRT; 198 AA.  
AC Q9BDC3;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE P27K1p1.  
GN P27K1p1.  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N A  
RX MEDLINE=21083196; PubMed=11115398;  
FA Hirano K., Hirano M., Zeng Y., Nishimura J., Hara K., Muta K.,  
RA Nawata H., Kanai H.;  
RT "Cloning and functional expression of a degradation-resistant novel  
RT isoform of p27K1p1";  
RL Biochem. J. 353:51-57(2001).  
DR EMBL; AB031957; BAB39727.1; -;  
DR EMBL; AB031955; BAB39725.1; -;  
DR EMBL; AB031956; BAB39726.1; -;  
DR InterPro; IPR003175; CDI.  
DR Flam; FF02234; CDI; 1.  
SQ SEQUENCE 198 AA; 22201 MW; E5B01D25E5BDD5F CRC64;

Query Match. 95.6%, Score 910, DB 6, Length 198,  
Best local similarity 95.5%, Pred. No. 1.5e-76;  
Matches 170; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Q7 1 MSNVRVNSGSPSLERMDARQAEYKESACPNLECFVNHPELTFDLEKHRDMEASQKRW 60  
|||||  
Q8 1 MSNVRVNSGSPSLERMDARQAEYKESACPNLECFVNHPELTFDLEKHRDMEASQKRW 60  
|||||  
Q9 61 NFDPQNHKPLEGKYEWQVEKGSLSPEFYYPYPPPPPKACAKVPAQESQDVSSTQAVPLMG 120  
|||||  
10 51 NFDPQNHKPLEGKYEWQVEKGSLSPEFYYPYPPPPPKACAKVPAQESQDVSSTQAVPLMG 120  
|||||

Q9QXHO rattus norv  
Q22198 caenorhabdi  
Q9HUS\* caenorhabdi  
Q22197 caenorhabdi  
Q8WQ2 drosophila  
Q04154 arabidopsis  
Q82809 arabidopsis  
P91554 drosophila  
Q03973 saccharomyc  
Q9VIC8 drosophila  
Q9KK24 streptococ  
Q94536 drosophila  
Q9FNE4 arabidopsis  
Q8F563 mus musculu  
Q9LMG1 arabidopsis  
Q9KK17 streptococ  
Q9KK37 streptococ  
P91668 drosophila  
Q93V92 nicotiana t  
Q9QZ47 mus musculu  
Q9QWT8 mus musculu  
Q94H57 oryza sativ  
Q9KK40 streptococ  
Q35613 mus musculu  
Q9FDQ1 streptococ  
Q99VK7 staphylococ  
Q91J15 arabidopsis  
Q93V23 arabidopsis  
Q9FS28 pisum sativ



RA Kawada M., Yamaguchi S., Kato S., Mizuno S., Uehara Y.,  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Kawada M., Yamaguchi S., Murakami Y., Suzuki K., Mizuno S., Uehara Y.,  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RA Dastvan F., Reidy M.A.,  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86924; BAA1660.1; -  
 DR EMBL: AF015194; AAB71368.1; -  
 DR InterPro: IPR003175; CDI.  
 DP Pfam: PF02234; CDI. 1.  
 SQ SEQUENCE 197 AA: 22112 MW: 5573807802098478 QPC64.

Query Match 88.2%; Score 840; DB 11; Length 197;  
 Best Local Similarity 87.8%; Pred. No. 4 e-70;  
 Matches 156; Conservative 10; Mismatches 12; Indels 0; Gaps 0.

QY 1 MSNVVNSGSPSLERMIAPCAAEYKPSACPNLFGPVNHFELIMLEKHPMPMEASQPKW 60  
 DB 1 MSNVVNSGSPSLERMIAPCAAEYKPSACPNLFGPVNHFELIMLEKHPMPMEASQPKW 60  
 QY 61 NFEUNHNPFLKGYEWKVEKGSLEPEYYPKPKKACVPAQESGVSTGCAVPLM; 120  
 DB 61 NFEUNHNPFLKGYEWKVEKGSLEPEYYPKPKKACVPAQESGVSTGCAVPLM; 120  
 QY 121 SCANSEDLHVDKTDADNCAGLAFCQCTGIRKPPATDSSPQNKRNPFTEENVSDGS 178  
 DB 121 SCANSEDLHVDKTDADNCAGLAFCQCTGIRKPPATDSSPQNKRNPFTEENVSDGS 178

RESULT 6  
 045792

ID 045792 PRELIMINARY; PRT; 197 AA  
 AC 03792;  
 DT 01-JAN-1998 (Tremblrel. 05, Created)  
 DI 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE P27.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Rattus  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SPLEEN;  
 RX MEDLINE=97361761; PubMed=9218722;  
 RA Nomura H., Sawada Y., Fujinaga K., Ohtaki S.,  
 RT "Cloning and characterization of rat p27Kip1, a cyclin dependent  
 kinase inhibitor."  
 RL Gene 191:211-218(1997).  
 DR EMBL: D83792; BAA21561.1; -  
 DR InterPro: IPR003175; CDI.  
 DP Pfam: PF02234; CDI. 1.  
 SQ SEQUENCE 197 AA: 22112 MW: 5573807802098478 QPC64.

Query Match 87.7%; Score 835; DB 11; Length 197;  
 Best Local Similarity 87.1%; Pred. No. 1.3e-65;  
 Matches 155; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 MSNVVNSGSPSLERMIAPCAAEYKPSACPNLFGPVNHFELIMLEKHPMPMEASQPKW 60  
 DB 1 MSNVVNSGSPSLERMIAPCAAEYKPSACPNLFGPVNHFELIMLEKHPMPMEASQPKW 60  
 QY 61 NFEUNHNPFLKGYEWKVEKGSLEPEYYPKPKKACVPAQESGVSTGCAVPLM; 120  
 DB 61 NFEUNHNPFLKGYEWKVEKGSLEPEYYPKPKKACVPAQESGVSTGCAVPLM; 120  
 QY 121 SCANSEDLHVDKTDADNCAGLAFCQCTGIRKPPATDSSPQNKRNPFTEENVSDGS 178  
 DB 121 SCANSEDLHVDKTDADNCAGLAFCQCTGIRKPPATDSSPQNKRNPFTEENVSDGS 178

LB 121 SCANSEDLHVDKTDADNCAGLAFCQCTGIRKPPATDSSPQNKRNPFTEENVSDGS 178

RESULT 7  
 Q9BEA5  
 ID Q9BEA5 PRELIMINARY; PRT; 172 AA.  
 AC Q9BEA5;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DI 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)  
 DE P27Kip1 degradation-resistant isoform (Fragment).  
 DR E27KIP1.  
 GS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina, Suidae, Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21063196; PubMed=11115398;  
 RA Hirano K., Hirano M., Zeng Y., Nishimura J., Hara K., Muta K.,  
 RA Nawata H., Kanaike H.;  
 RT "Cloning and functional expression of a degradation-resistant novel  
 isoform of p27Kip1."  
 FL Biochem. J. 344:51-57(2001)  
 DR EMBL: AB031958; BAB39728.1; -  
 DR InterPro: IPR002047; AKH.  
 DR InterPro: IPR003175; AKH.  
 DP Pfam: PF02234; CDI. 1.  
 DR PROSITE: PS00256; AKH; UNKNOWN\_1.  
 FT NON-TER; 1  
 SQ SEQUENCE 172 AA: 19348 MW: 98822408844466 QPC64;

Query Match 83.1%; Score 791; DB 6; Length 172;  
 Best Local Similarity 94.8%; Pred. No. 1.3e-65;  
 Matches 146; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 9 GSPSLERMIAPCAAEYKPSACPNLFGPVNHFELIMLEKHPMPMEASQPKWDFQNHK 68  
 DB 1 GSPSLERMIAPCAAEYKPSACPNLFGPVNHFELIMLEKHPMPMEASQPKWDFQNHK 60  
 QY 69 PLEGKVEWKEVEKGSLEPEYYPKPKKACVPAQESGVSTGCAVPLMGSQANSEDT 128  
 DB 61 PLEGKVEWKEVEKGSLEPEYYPKPKKACVPAQESGVSTGCAVPLMGSQANSEDT 120  
 QY 129 HLIVLKEITADNCAGLAFCQCTGIRKPPATDSSP 162  
 DB 121 HLIVLKEITADNCAGLAFCQCTGIRKPPATDSSP 154

RESULT 8

ID 043806 PRELIMINARY; PRT; 158 AA  
 AC 043806;  
 DT 01-JUN-1998 (Tremblrel. 06, Created)  
 DI 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE P27 Kip1 protein (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A  
 RC TISSUE=REAST; CARCINOMA;  
 RX MEDLINE=96140757; PubMed=8557269;  
 RA Ferrando A., Balbin M., Pendas A.M., Vizoso F., Velasco G.,  
 RA Lopez-otin C.;  
 RT "Mutational analysis of the human cyclin-dependent kinase inhibitor  
 p27 Kip1 in primary breast carcinomas."  
 RL Hum. Genet. 97:91-94(1996).  
 DP EMBL: X84849; CAA59284.1; -  
 DR InterPro: IPR003175; CDI.

QY 9 GSPSLERMIAPCAAEYKPSACPNLFGPVNHFELIMLEKHPMPMEASQPKWDFQNHK 68  
 DB 1 GSPSLERMIAPCAAEYKPSACPNLFGPVNHFELIMLEKHPMPMEASQPKWDFQNHK 60  
 QY 69 PLEGKVEWKEVEKGSLEPEYYPKPKKACVPAQESGVSTGCAVPLMGSQANSEDT 128  
 DB 61 PLEGKVEWKEVEKGSLEPEYYPKPKKACVPAQESGVSTGCAVPLMGSQANSEDT 120  
 QY 129 HLIVLKEITADNCAGLAFCQCTGIRKPPATDSSP 162  
 DB 121 HLIVLKEITADNCAGLAFCQCTGIRKPPATDSSP 154



```

DB 10 EEMISAFVAVLPRKLSAGIGAGACPNLPFPHHGMFSELPKLNELTASLQWKNFDEP 69
QY 68 KPLGKQVWQVKECSIPEFYPPRPFKCAKVPAGESLVSZTPGCAVILMSQANSE 127
DB 70 TPLKGIETWPEVSEKMPSEYQNPSTAAANTTSPEQQ-QPLLSVQPEP--PEEAPVD 126
QY 128 THLYDQKTDADNCAAGLAEQCTGTRPKPPATITSPQNKRPANP 169
DB 127 VNVNENPCAKFNFAKIVKPKQGVF--GPAFASANISLTPKPK 167

RESULT 12
Q91V06
ID Q91V06 PRELIMINARY; PRT; 335 AA.
AC Q91V06;
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DI 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 25, Last annotation update)
DE Cyclin dependent kinase inhibitor 1C (p57kip2 protein) (P57).
GN CDKN1C OR p57kip2.
OS Mus musculus domesticus (western European house mouse), and
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10097; 10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.musculus domesticus; STRAIN=129 SV;
RX MEDLINE=20519229; PubMed=11061728;
RA Engemann S.; Stroedter M.; Paulsen M.; Frank G.; Reinhardt P.;
RA Lane N.; Reik W.; Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
RT implications for a novel imprinting centre and extended imprinting."
PL Hum. Mol. Genet. 9:2691-2706(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.musculus domesticus; STRAIN=129 SV;
RA Engemann S.;
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=129/SV;
RX MEDLINE=20014712; PubMed=10545601;
RA John R.M., Hodges M., Little P., Barton S.C., Surani M.A.;
RT "A human p57kip2 transgene is not activated by passage through the
RT maternal mouse germline."
PL Hum. Mol. Genet. 8:2211-2219(1999)
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; TISSUE=HEPAST TUMOR;
RA Strausberg R.;
RX Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
DR EMBL: AJ276505; AAC16402.1;
DR EMBL: AF160190; AAF00984.1;
DR EMBL: BC005412; AAH05412.1;
DR MGD: MGI:104564; Cdkn1c;
DR InterPro: IPR003175; CDI;
DR Pfam: PF02234; CDI; 1.
KW Kinase.
SQ SEQUENCE 335 AA: 3500 MW: 4504676287FERGF CPG64;
Query Match 20.1%; Score 191.5; DB 11; Length 335;
Best Local Similarity 31.6%; Pred. No. 9.2e-10;
Matches 54; Conservative 24; Mismatches 52; Indels 41; Gaps 7;

QY 13 LERMTAGAEYF KFSATENIPGVNHFPTFTCLEKHEFFEFASQKWNTEFNKIF 69
DB 1 MERL-ASSDTPVVIARSACHSLFGVPVDHDELGRMLRLAELNAELDNWDFNQDVP 59
QY 70 LE--GKYVWQVFKGSIPEFYPP-----PPPKGACKV-----PAGESQVDS 110
DB 60 LRGPRGQWMEVDSVFAEYFETVQVWVPLGLGPPPPVAVAVIFRSPPFAEAPD-- 117
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QY 111 GTFQAVPLMSQANSETHLVKRTITAINAGLAEQCTGTRPKPPATITSS 161
DB 118 GLEEA-----PEQPPSAPASVAEPTPPATPAPASDLTS 152

RESULT 13
Q64315
ID Q64315 PRELIMINARY; PRT; 164 AA.
AC Q64315;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE P21 (WAF1).
GN WAF1 OR CIP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95316868; PubMed=7756420;
RA el-Deiry W.S.; Tokino T.; Waldman T.; Velculescu V.; Oliner J.D.;
RA Burrell M.; Hill D.E.; Fees J.L.; Hamilton S.F.; Kinzler K.W.;
RA Vogelstein B.;
RT "Topological control of p21WAF1/CIP1 expression in normal and
RT neoplastic tissues."
KL Cancer Res. 55:2910-2919(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX SIFAIN=F44/N; TISSUE=LUNG;
RA Belinsky S.A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
DR EMBL: U24174; AAC5221.1;
DR EMBL: L41275; AAC42084.1;
DR InterPro: IPR003175; CDI;
DR Pfam: PF02234; CDI; 1.
SQ SEQUENCE 164 AA: 6057E86045E6435F CPG64;
Query Match 19.6%; Score 187; DB 11; Length 164;
Best Local Similarity 26.9%; Pred. No. 9.9e-10;
Matches 43; Conservative 25; Mismatches 66; Indels 26; Gaps 3;

QY 17 LAFQAHYPKFSATPNLFGPVNHEELTFLFKIPPRMEFASQKWNTEFNHXPLEGKYEW 76
DB 6 EVRPVPH-RSKVCRKLFGVDSEQSPDCDALMSCLQPARERWNPDFATETPLEGNYW 64
QY 77 QEVEKSLPEFYFPEPEPKGA-KVIAQESQVSGTFQAVPLMSQANSETHLYDQKTD 136
DB 65 FQVPSPLPKVLSL-----GSKPKULGQKPPSTSSALIGGPGP 105
QY 137 TAINAGLAEQCTGTRPKPPATITSSP-----QNKRPANP 170
DB 106 APEDHVALSLSCTIVSHAPERPPDPSPGSGTSTSGRKRPT 145

RESULT 14
Q9UH60
ID Q9UH60 PRELIMINARY; PRT; 42 AA.
AC Q9UH60;
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DI 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Cyclin-dependent kinase inhibitor p27 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Walitregny D.; Loda M.;
RT "Homo sapiens cyclin-dependent kinase inhibitor p27 intron."
KL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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Genome version 5.1.5  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 08:52:12 ; Search time 14 718 Seconds  
(without alignments)  
606.682 Million cell updates/sec

Title: US-09-865-018b-6\_copy\_22\_88

Perfect score: 378  
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Scoring table: BLOSUM62

Gapop 10 0 ; Gapext 0 5

Searched: 908476 seqs, 13250620 residues

Total number of hits satisfying chosen parameters: 908476

Minimum DH seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A\_Geneset\_101002.\*

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23: /SIDS2/gcadata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	378	100.0	178	AA199131	Mink kipl, p27-kipl
2	378	100.0	178	AA1992707	Mink p27 kipl part
3	378	100.0	178	AA1992719	Partial 27 kda pro
4	370	97.9	172	AA1991588	Porcine p27kipl po
5	370	97.9	172	AA1991589	Porcine p27kipl po
6	360	95.2	167	AA1995101	Truncated p27 prot
7	360	95.2	177	AA1997530	Truncated Human p2
8	360	95.2	177	AA1996072	Human truncated cy
9	360	95.2	177	AA1996072	Human cyclin depen
10	360	95.2	194	AA1994930	Amino acid sequenc

11	360	95.2	198	AA199133	Human kipl, p27-ki
12	360	95.2	198	AA1992709	Human p27 kipl. H
13	360	95.2	198	AA1992717	27 kda protein inh
14	360	95.2	198	AA1996888	Amino acid sequenc
15	360	95.2	198	AA19900768	CKI/KIP protein p2
16	360	95.2	198	AA1997523	Human p27 protein
17	360	95.2	198	AA1996052	Human cyclin depen
18	360	95.2	198	AA1996066	Human cyclin depen
19	360	95.2	198	AA19970307	Human mutant cycli
20	360	95.2	198	AA19944400	Human p27(kipl) ki
21	360	95.2	198	AA1994449	Amino acid sequenc
22	360	95.2	198	AA19948309	Human p27 protein
23	360	95.2	198	AA19948309	Human p27 protein
24	360	95.2	198	AA19948309	Human p27 protein
25	360	95.2	198	AA19948309	Human p27 protein
26	360	95.2	198	AA19948309	Human p27 protein
27	360	95.2	198	AA19948309	Human p27 protein
28	360	95.2	198	AA19948309	Human p27 protein
29	360	95.2	198	AA19948309	Human p27 protein
30	360	95.2	198	AA19948309	Human p27 protein
31	360	95.2	198	AA19948309	Human p27 protein
32	360	95.2	198	AA19948309	Human p27 protein
33	360	95.2	198	AA19948309	Human p27 protein
34	360	95.2	198	AA19948309	Human p27 protein
35	360	95.2	198	AA19948309	Human p27 protein
36	360	95.2	198	AA19948309	Human p27 protein
37	360	95.2	198	AA19948309	Human p27 protein
38	360	95.2	198	AA19948309	Human p27 protein
39	360	95.2	198	AA19948309	Human p27 protein
40	360	95.2	198	AA19948309	Human p27 protein
41	360	95.2	198	AA19948309	Human p27 protein
42	360	95.2	198	AA19948309	Human p27 protein
43	360	95.2	198	AA19948309	Human p27 protein
44	360	95.2	198	AA19948309	Human p27 protein
45	360	95.2	198	AA19948309	Human p27 protein

#### ALIGNMENTS

RESULT 1  
AA199131 standard; protein, 178 AA.  
AA199131  
AC AA199131:  
DT 27-FEB-1996 (first entry)  
DE Mink kipl, p27-kipl or p27, cyclin E-Cdk2 activation inhibitor.  
KW Mink kipl, p27-kipl, p27, cyclin E-Cdk2 complex, cancer;  
KW activation inhibitor, hyperplasia; cyclin dependent kinase;  
KW diagnosis, hyperproliferative disorder; ulcer; partial protein.  
XX Mustela vison.  
OS  
XX  
XX Key Location/Qualifiers  
FT Peptide 31..43  
FT /note= "obtd. from purified kipl, and  
FT used to design degenerate oligo-  
FT nucleotide PCR primer"  
FT Peptide 74..79  
FT /note= "obtd. from purified kipl, and  
FT used to design degenerate oligo-  
FT nucleotide PCR primer"  
FT Peptide 83..96  
FT /note= "obtd. from purified kipl"  
FT Peptide 114..122  
FT /note= "obtd. from purified kipl"  
FT Peptide 135..147  
FT /note= "obtd. from purified kipl"  
XX  
PN W09518824-A1.

[illegible][illegible]

PT especially breast carcinoma  
 XX  
 PS Disclosure; Fig 13b; 105pp; English.  
 XX  
 CC The present sequence represents a partial 27 kDa protein (p27 or Kip1)  
 CC which inhibits the activation of a cyclin E-cyclin-dependent kinase2  
 CC (Cdk2) complex. A reduced relative level of kip1 is indicative of a  
 CC hyperproliferative disease (particularly cancer, especially breast  
 CC carcinoma) and also is prognostic for increased risk of death and/or  
 CC recurrence of cancer (and may be used to determine suitable treatments).  
 CC Agents that affect the activity of kip1 can be used to treat  
 CC hyperproliferative conditions, e.g. to stimulate tissue or organ repair  
 CC or to establish cell cultures.  
 XX  
 SQ Sequence 178 AA;  
 Query Match 100.0%; Score 378; DB 19; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-41;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EYKPSACRNLFQGVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 60  
 DB 22 EYKPSACRNLFQGVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 81  
 QY 61 GSLPEFY 67  
 DB 82 GSLPEFY 88  
 RESULT 4  
 AAM51588 standard; Protein; 172 AA.  
 ID AAM51588  
 AC AAM51588;  
 DT 01-FEB-2002 (first entry)  
 XX Porcine p27Kip1 polypeptide #1.  
 DE Pig, antiarteriosclerotic; cytostatic; gene therapy; p27Kip1;  
 KW proteasome decomposition resistance; cancer; arteriosclerosis.  
 XX  
 OS Sus scrofa.  
 XX JP2001258561-A  
 PN 25-SEP-2001.  
 XX  
 PD 17-MAR-2000; 2000JP-0076840.  
 XX  
 PF 17-MAR-2000; 2000JP-0076840.  
 XX  
 PR 17-MAR-2000; 2000JP-0076840.  
 XX  
 PA (UYKY-) UNIV KYUSHU.  
 XX  
 DP WPI; 2002-003329/01  
 DR N-PSDB; ABA01079.  
 XX  
 PT Nucleic acid and amino acid sequence for showing resistance against  
 PT proteasome decomposition, comprises a new p27Kip1 molecular species -  
 XX  
 PS Disclosure; Page 6-7; 12pp; Japanese.  
 XX  
 CC The invention relates to a novel p27Kip1 polynucleotide and protein  
 CC The p27Kip1 protein shows resistance to proteasome decomposition  
 CC and can be used in the treatment of cancers and arteriosclerosis. The  
 CC invention also relates to a recombinant vector containing the  
 CC polynucleotide, and to a transformant containing the recombinant  
 CC vector. The present sequence is the polypeptide of the invention.  
 XX  
 SQ Sequence 172 AA;  
 Query Match 97.9%; Score 370; DB 23; Length 172;  
 Best Local Similarity 98.5%; Pred. No. 4.5e-40;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EYKPSACRNLFQGVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 60  
 DB 14 EYKPSACRNLFQGVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 73  
 QY 61 GSLPEFY 67  
 DB 74 GSLPEFY 80  
 RESULT 5  
 AAM51589 standard; Protein; 198 AA.  
 ID AAM51589  
 AC AAM51589;  
 DT 01-FEB-2002 (first entry)  
 XX Porcine p27Kip1 polypeptide #2.  
 DE Pig, antiarteriosclerotic; cytostatic; gene therapy; p27Kip1;  
 KW proteasome decomposition resistance; cancer; arteriosclerosis.  
 XX  
 OS Sus scrofa.  
 XX JP2001258561-A  
 PN 25-SEP-2001.  
 XX  
 PD 17-MAR-2000; 2000JP-0076840.  
 XX  
 PF 17-MAR-2000; 2000JP-0076840.  
 XX  
 PR (UYKY-) UNIV KYUSHU.  
 XX  
 DR WPI; 2002-003329/01.  
 DR N-PSDB; ABA01080.  
 XX  
 PT Nucleic acid and amino acid sequence for showing resistance against  
 PT proteasome decomposition, comprises a new p27Kip1 molecular species -  
 XX  
 PS Disclosure; Page 8-9; 12pp; Japanese.  
 XX  
 CC The invention relates to a novel p27Kip1 polynucleotide and protein  
 CC The p27Kip1 protein shows resistance to proteasome decomposition  
 CC and can be used in the treatment of cancers and arteriosclerosis. The  
 CC invention also relates to a recombinant vector containing the  
 CC polynucleotide, and to a transformant containing the recombinant  
 CC vector. The present sequence is a p27Kip1 polypeptide.  
 XX  
 SQ Sequence 198 AA;  
 Query Match 97.9%; Score 370; DB 23; Length 198;  
 Best Local Similarity 98.5%; Pred. No. 5.4e-40;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EYKPSACRNLFQGVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 60  
 DB 22 EYKPSACRNLFQGVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 81  
 QY 61 GSLPEFY 67  
 DB 82 GSLPEFY 88  
 RESULT 6  
 AAW95101 standard; Protein; 167 AA.  
 ID AAW95101  
 AC AAW95101;  
 DT 25-MAY-1999 (first entry)







XX Sequence 198 AA;  
 Query Match 95.2%; Score 460; DB 16; Length 198;  
 Best Local Similarity 95.5%; Pred. No. 1 le-38;  
 Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLFPGPVNHEELTRDLEKHHRDMEASQKWNFDQNHKPLEGKYEWQVEK 60  
 DB 22 EHPKPSACRNLFPGPVNHEELTRDLEKHHRDMEASQKWNFDQNHKPLEGKYEWQVEK 81  
 QY 61 GSLPEFY 67  
 DB 82 GSLPEFY 88

RESULT 12  
 ID AAR92709 standard; Protein: 198 AA.  
 XX AAR92709;  
 DT 16-JUL-1996 (first entry)  
 XX Human p27 Kip1.  
 XX p27 protein, Kip1, cyclin E, Cdk2, cell proliferation, cancer,  
 KW cancer; hyperplasia; diagnosis; therapy.  
 XX Homo sapiens.  
 XX W09602140-A1.  
 XX 01-FEB-1996.  
 XX 07-JUN-1995; 95WO-US07361.  
 XX 15-JUL-1994; 94US-0275943  
 XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 PA (SLOK) SLOAN FETTERING INST CANCER RES.  
 XX Koff A, Massague J, Polyak K, Roberts JM;  
 WPI: 1996-105553/11.  
 DR N-PSDB; AAT16336.  
 XX p27, an inhibitor of cyclin E-Cdk2 complex activation, and agents  
 PT which enhance and inhibit its activity, useful for treating  
 PT hyper proliferative and hypo proliferative disorders  
 XX Disclosure; Fig 15a-b; 129pp; English.  
 XX A cDNA clone (AAT16336) derived from human kidney codes for a 27  
 CC kDa protein, p27 Kip1 (AAR92709), that is capable of binding to  
 CC and inhibiting the activation of a cyclin E-Cdk2 complex. Human  
 CC Kip1 shows a high degree of homology to p107 (AAR92707) and p130  
 CC (AAR92708) Kip1 proteins, and the N-terminal half of the protein shows  
 CC significant homology to Cipl/WAF1. Kip1 shows weak inhibitory  
 CC activity and prevents cdk2 activation. Overexpression inhibits  
 CC cell entry to the S phase. Kip1 can be produced by expression of  
 CC the cDNA clone in cultured cells. It can be used in vitro  
 CC assays to screen agents that affect p27 activity, and in methods  
 CC for the diagnosis and treatment of hyperproliferative disorders,  
 CC e.g. cancer, and hyperproliferative disorders, e.g. cancer and  
 CC hyperplasia.  
 XX Sequence 198 AA;  
 Query Match 95.2%; Score 360; DB 17; Length 198,  
 Best Local Similarity 95.5%; Pred No 1 le-38;  
 Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLFPGPVNHEELTRDLEKHHRDMEASQKWNFDQNHKPLEGKYEWQVEK 60  
 DB 22 EHPKPSACRNLFPGPVNHEELTRDLEKHHRDMEASQKWNFDQNHKPLEGKYEWQVEK 81  
 QY 61 GSLPEFY 67  
 DB 82 GSLPEFY 88

RESULT 13  
 ID AAW29717 standard; Protein: 198 AA.  
 XX AAW29717;  
 AC AAW29717;  
 DT 27-OCT-1998 (first entry)  
 XX 27 kDa protein inhibiting activation of cyclin E-Cdk2 complex.  
 DE 27 kDa protein; p27; Kip1, inhibit, activation, cancer, breast carcinoma;  
 KW cyclin E-cyclin-dependent kinase2 complex; hyperproliferative disease;  
 KW recurrence; treatment; human.  
 XX Homo sapiens.  
 OS W09834121-A2.  
 PN 06-AUG-1998.  
 XX 03-FEB-1998; 98WO-US01893.  
 XX 03-FEB-1997; 97US-0794002.  
 XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 PA Porter PL, Roberts JM;  
 PI WPI: 1998-437612/37.  
 DR N-PSDB; AAV47517.  
 XX Assays for protein p27 inhibiting activation of cyclin E-Cdk2  
 PT complex, useful for, e.g. diagnosis and prognosis of cancer,  
 PT especially breast carcinoma  
 XX Claim 18; Fig 15B; 105pp; English.  
 XX The present sequence represents a 27 kDa protein (p27 or Kip1) which  
 CC inhibits the activation of a cyclin E-cyclin dependent kinase2 (Cdk2)  
 CC complex. A reduced relative level of Kip1 is indicative of a  
 CC hyperproliferative disease (particularly cancer, especially breast  
 CC carcinoma) and also is prognostic for increased risk of death and/or  
 CC recurrence of cancer (and may be used to determine suitable treatments).  
 CC Agents that affect the activity of Kip1 can be used to treat  
 CC hyperproliferative conditions, e.g. to stimulate tissue or organ repair  
 CC or to establish cell cultures.  
 XX Sequence 198 AA;  
 Query Match 95.2%; Score 360; DB 17; Length 198;  
 Best Local Similarity 95.5%; Pred. No. 1 le-38;  
 Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLFPGPVNHEELTRDLEKHHRDMEASQKWNFDQNHKPLEGKYEWQVEK 60  
 DB 22 EHPKPSACRNLFPGPVNHEELTRDLEKHHRDMEASQKWNFDQNHKPLEGKYEWQVEK 81  
 QY 61 GSLPEFY 67  
 DB 82 GSLPEFY 88

RESULT 14  
 AAW46888





GenCore version 5.1.6  
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OM protein protein search, using sw model

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(without alignments)  
392.644 Million cell updates/sec

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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6: /seq2.6/ptdata/1/iaa/EA\_CMR pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	378	100.0	178	4	US-08-794-002-6
2	378	100.0	178	4	US-08-854-039B-6
3	378	100.0	198	1	US-08-275-983B-1
4	378	100.0	198	4	US-08-794-002-2
5	360	95.2	177	4	US-03-457-568-12
6	360	95.2	177	4	US-09-457-568-12
7	360	95.2	198	1	US-08-457-646-16
8	360	95.2	198	1	US-08-406-248-4
9	360	95.2	198	4	US-08-897-333A-2
10	360	95.2	198	4	US-08-240-068-6
11	360	95.2	198	4	US-08-794-002-2
12	360	95.2	198	4	US-09-457-568-12
13	360	95.2	198	4	US-09-457-568-12
14	360	95.2	334	4	US-09-457-568-16
15	360	95.2	334	4	US-09-457-646-16
16	360	95.2	348	4	US-09-457-568-14
17	360	95.2	348	4	US-09-457-646-14
18	360	95.2	365	4	US-09-457-568-10
19	360	95.2	365	4	US-09-457-568-10
20	360	95.2	365	4	US-09-457-646-10
21	360	95.2	365	4	US-09-457-646-10
22	360	95.2	380	4	US-09-457-568-8
23	360	95.2	380	4	US-09-457-646-8
24	360	95.2	391	1	US-08-589-981-2
25	360	95.2	391	4	US-09-457-568-4
26	360	95.2	391	4	US-09-457-646-4
27	357	94.4	198	4	US-08-854-039B-2

Sequence 2, Appli  
Sequence 8, Appli  
Sequence 57, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 18, Appli  
Sequence 18, Appli  
Sequence 20, Appli  
Sequence 20, Appli  
Sequence 20, Appli  
Sequence 22, Appli  
Sequence 22, Appli  
Sequence 6, Appli  
Sequence 30, Appli  
Sequence 56, Appli  
Sequence 56, Appli  
Sequence 53, Appli  
Sequence 52, Appli  
Sequence 49, Appli

ALIGNMENTS

RESULT 1  
US-08-794-002-6  
: Sequence 6, Application US/08794002  
: Patent No. 6316208  
: GENERAL INFORMATION:  
: APPLICANT: Roberts, James M.  
: APPLICANT: Porter, Peggy L.  
: TITLE OF INVENTION: ISOLATED P-7 PROTEIN AND METHODS FOR ITS  
: TITLE OF INVENTION: PRODUCTION AND USE  
: NUMBER OF SEQUENCES: 23  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: FOLEY, HOAG & ELLIOT LLP  
: STREET: One Post Office Square  
: CITY: Boston  
: STATE: MA  
: COUNTRY: USA  
: ZIP: 02109-2170  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent in Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/794,002  
: FILING DATE: 03-FEB-1997  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Vincent, Matthew P.  
: REGISTRATION NUMBER: 36,709  
: REFERENCE/DOCKET NUMBER: MIV-079, 03  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 617-832-1009  
: TELEFAX: 617-832-7000  
: INFORMATION FOR SEQ ID NO: 6:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 178 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
US-08-794-002-6

Query Match: 100.0% Score: 378 DB: 4 Length: 178  
Best Local Similarity: 100.0% P-7 N: 1.7e-41  
Matches: 67; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
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DB: 22 EYPKPSACNLFQVNHHEELTRLEKHKRDMKMEASQKWNFQVNHKPLPKYKFWVEVK 81  
Q7: 61 GSLPEFY 67



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;
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-794-002-22
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; Query Match 100.0% Score 378; DB 4; Length 198,
; Best Local Similarity 100.0%; Pred. No. 1.9e-41;
; Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 22 EYPKPSACNLFGPVNHEELTRDLKRRDMEESQKKNFDFONHKPLEGKYEWQVEVK 81
;
QY 61 GSLPEFY 67
Db 82 GSLPEFY 88
;
;
; RESULT 5
; US-09-457-568-12
; Sequence 12, Application US/09457568
; Patent No. 6413943
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jenő
; APPLICANT: Finer, Mitchell H
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; TITLE OF INVENTION: Smooth Muscle Cells
; FILE REFERENCE: 106482.691
; CURRENT APPLICATION NUMBER: US/09/457,568
; EARLIER FILING DATE: 1993-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 12
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-568-12
;
;
; Query Match 95.2% Score 360; DB 4; Length 177;
; Best Local Similarity 95.5%; Pred. No. 3.7e-39;
; Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 EYPKPSACNLFGPVNHEELTRDLKRRDMEESQKKNFDFONHKPLEGKYEWQVEVK 60
Db 22 EYPKPSACNLFGPVNHEELTRDLKRRDMEESQKKNFDFONHKPLEGKYEWQVEVK 81
;
QY 61 GSLPEFY 67
Db 82 GSLPEFY 88
;
;
; RESULT 6
; US-09-457-646-12
; Sequence 12, Application US/09457646
; Patent No. 6420345
; GENERAL INFORMATION:
; APPLICANT: Patel, Salil D
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jenő
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;
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; TITLE OF INVENTION: Smooth Muscle Cells
; FILE REFERENCE: 106482.287
; CURRENT APPLICATION NUMBER: US/09/457,646
; EARLIER FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 12
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-646-12
;
;
; Query Match 95.2% Score 360; DB 4; Length 177;
; Best Local Similarity 95.5%; Pred. No. 3.7e-39;
; Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
;
QY 1 EYPKPSACNLFGPVNHEELTRDLKRRDMEESQKKNFDFONHKPLEGKYEWQVEVK 60
Db 22 EYPKPSACNLFGPVNHEELTRDLKRRDMEESQKKNFDFONHKPLEGKYEWQVEVK 81
;
QY 61 GSLPEFY 67
Db 82 GSLPEFY 88
;
;
; RESULT 7
; US-08-275-983B-3
; Sequence 3, Application US/08275983B
; Patent No. 5688665
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Kof, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Isolated p27 protein, Nucleic Acid Molecules
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,983B
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/179,045
; FILING DATE: 07-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: M11-079CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; TITLE OF INVENTION: PRODUCTION AND USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,002
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079,03
; TELEPHONE: 617-832-1000
; TELEFAX: 617-842-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-794-002-2

Query Match 95.2%; Score 360; DB 4; Length 198;
Best Local Similarity 95.5%; Pred. No. 4.2e-39;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 61 GSLPEFY 67
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Db 82 GSLPEFY 88

RESULT 12
US-09-457-568-26
; Sequence 26, Application US/09457568
; Patent No. 6413943
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jeno
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; FILE REFERENCE: 106482.691
; CURRENT APPLICATION NUMBER: US/09/457,568
; CURRENT FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-568-26

Query Match 95.2%; Score 360; DB 4; Length 198;
Best Local Similarity 95.5%; Pred. No. 4.2e-39;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYPKPSACRNLFPGVNVNHEELTRDLKHKHRTMFECSPKWNFTDFONHKPLEGKYEQVEVK 60
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Db 22 EHPKPSACRNLFPGVDHHEELTRDLKHKHCRDMEASQKWNFDQNHKPLEGKYEQVEVK 81
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QY 61 GSLPEFY 67
|:|||||
Db 82 GSLPEFY 88

RESULT 13
US-09-457-646-26
; Sequence 26, Application US/09457646
; Patent No. 6420345
; GENERAL INFORMATION:
; APPLICANT: Patel, Salil D
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jeno
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; FILE REFERENCE: 106482.287
; CURRENT APPLICATION NUMBER: US/09/457,646
; CURRENT FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-646-26

Query Match 95.2%; Score 360; DB 4; Length 198;
Best Local Similarity 95.5%; Pred. No. 4.2e-39;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYPKPSACRNLFPGVNVNHEELTRDLKHKHRTMFECSPKWNFTDFONHKPLEGKYEQVEVK 60
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Db 22 EHPKPSACRNLFPGVDHHEELTRDLKHKHCRDMEASQKWNFDQNHKPLEGKYEQVEVK 81
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QY 61 GSLPEFY 67
|:|||||
Db 82 GSLPEFY 88

RESULT 14
US-09-457-568-16
; Sequence 16, Application US/09457568
; Patent No. 6413943
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jeno
; APPLICANT: Finer, Mitchell H
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; FILE REFERENCE: 106482.691
; CURRENT APPLICATION NUMBER: US/09/457,568
; CURRENT FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-568-16
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Computer Ltd.

OM protein protein search, using sw model

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(without alignments)  
991.736 Million col: updates/sec

Title: US-09-865-018b-6\_COPY\_22\_88

Perfect score: 478

Sequence: 1 EYPKDSACPNIFGPVNHPEI

Scoring table: BLOSUM62 PILEUPWEVEKRS[PPFY 67

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Searched: 383516 seqs, 101223644 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

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- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB pep:\*
- 3: /cgn2\_6/prodata/1/pubpaa/us06\_NEW\_PUB pep:\*
- 4: /cgn2\_6/prodata/1/pubpaa/us06\_PUBCOMB pep:\*
- 5: /cgn2\_6/prodata/1/pubpaa/us07\_NEW\_PUB pep:\*
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- 11: /cgn2\_6/prodata/1/pubpaa/us10\_NEW\_PUB pep:\*
- 12: /cgn2\_6/prodata/1/pubpaa/us10\_PUBCOMB pep:\*
- 13: /cgn2\_6/prodata/1/pubpaa/us03\_NEW\_PUB pep:\*
- 14: /cgn2\_6/prodata/1/pubpaa/us06\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	378	100	0	178	US-09-865-018-6 Sequence 6, Appli
2	369	95.2	167	8	US-08-902-572-18 Sequence 18, Appli
3	360	95.2	169	9	US-09-970-561-2 Sequence 2, Appli
4	360	95.2	334	8	US-08-902-572-22 Sequence 22, Appli
5	360	95.2	348	8	US-08-902-572-24 Sequence 24, Appli
6	360	95.2	365	8	US-08-902-572-8 Sequence 8, Appli
7	360	95.2	380	8	US-08-902-572-6 Sequence 6, Appli
8	360	95.2	391	8	US-08-902-572-2 Sequence 2, Appli
9	357	94.4	198	10	US-09-865-018-2 Sequence 2, Appli
10	356	94.2	197	10	US-09-865-018-4 Sequence 4, Appli
11	354	93.7	237	8	US-08-902-572-26 Sequence 26, Appli
12	354	93.7	252	8	US-08-902-572-28 Sequence 28, Appli
13	346	91.5	70	8	US-08-902-572-20 Sequence 20, Appli
14	148	39.2	164	9	US-09-221-268-4 Sequence 3, Appli
15	148	39.2	164	9	US-09-221-268-5 Sequence 5, Appli
16	148	39.2	164	10	US-09-865-018-24 Sequence 24, Appli
17	148	39.2	164	10	US-09-940-766-2 Sequence 2, Appli
18	145	38.4	247	10	US-09-925-237-770 Sequence 770, App
19	100	26.5	191	10	US-09-733-507-2 Sequence 2, Appli

20	100	26.5	191	10	US-09-733-507-10	Sequence 10, Appli
21	81.5	21.6	213	10	US-09-733-507-12	Sequence 12, Appli
22	81	21.4	137	10	US-09-733-507-14	Sequence 14, Appli
23	71.5	18.9	196	10	US-09-733-507-16	Sequence 16, Appli
24	71	18.8	13	10	US-09-865-018-26	Sequence 26, Appli
25	71	18.8	208	10	US-09-733-507-13	Sequence 13, Appli
26	67.5	17.6	176	10	US-09-733-507-11	Sequence 11, Appli
27	66.5	17.6	190	9	US-09-993-308-4	Sequence 4, Appli
28	66	17.5	133	10	US-09-865-018-27	Sequence 27, Appli
29	65.5	17.3	147	9	US-10-219-220-173	Sequence 173, App
30	65	17.2	746	9	US-10-153-668-232	Sequence 232, App
31	61	16.1	282	9	US-09-845-713A-2	Sequence 2, Appli
32	60.5	16.0	373	9	US-10-219-220-285	Sequence 285, App
33	60.5	16.0	396	9	US-10-219-220-153	Sequence 153, App
34	60	15.9	317	9	US-09-925-299-853	Sequence 853, App
35	60	15.9	317	10	US-09-925-299-853	Sequence 853, App
36	60	15.9	552	4	US-09-819-142-22	Sequence 22, Appli
37	60	15.9	770	9	US-10-153-668-7	Sequence 7, Appli
38	60	15.9	770	9	US-10-153-668-452	Sequence 452, App
39	59.5	15.7	1267	9	US-10-059-585-56	Sequence 56, Appli
40	59	15.6	764	9	US-09-854-133-67	Sequence 67, Appli
41	59	15.6	764	10	US-09-738-973-67	Sequence 67, Appli
42	59	15.6	934	9	US-10-072-036-137	Sequence 137, App
43	59	15.6	933	9	US-10-072-036-135	Sequence 135, App
44	58	15.5	267	9	US-09-903-308-2	Sequence 2, Appli
45	58.5	15.5	474	10	US-09-529-063-40	Sequence 40, Appli

ALIGNMENTS

RESULT 1

US-09-865-018-6

: Sequence b, Application US/09865018

: Patent No. US20020110886A1

: GENERAL INFORMATION:

: APPLICANT: Massague, Joan

: Roberts, James M.

: Koff, Andrew

: Pelyak, Kornelia

: TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS

: PRODUCTION AND USE

: NUMBER OF SEQUENCES: 27

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: FOLEY, HOAG & ELIOT LLP

: STREET: One Post Office Square

: CITY: Boston

: STATE: MA

: COUNTRY: USA

: ZIP: 02109-2170

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent In Release: #1.0, Version #1.30

: CURRENT APPLICATION DATA: US/09/865,018

: APPLICATION NUMBER: US/09/865,018

: FILING DATE: 24-May-2001

: PRIORITY DATA:

: APPLICATION NUMBER: US/08/854,039

: FILING DATE: 09-MAY-1997

: ATTORNEY/AGENT INFORMATION

: NAME: Vincent, Matthew P.

: REGISTRATION NUMBER: 36,709

: REFERENCE/DOCKET NUMBER: MIV-079.04

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 617-832-1000

: TELEFAX: 617-832-7090

: INFORMATION FOR SEQ ID NO: 6:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 178 amino acids

: TYPE: amino acid

: TOPOLOGY: linear









Db 22 EOPKPSACNPLGPDVHEELTRDLKKHCRDMEASQRKWNFDQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67

|||||

Db 82 GSLPEFY 88

## RESULT 10

US-09-865-018-4

; Sequence 4, Application US/09865018

; Patent No. US2002011044A1

; GENERAL INFORMATION:

; APPLICANT: Massague, Joan

; Kofl, Andrew

; Polyak, Kornelia

; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS

; PRODUCTION AND USE

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/865,018

; FILING DATE: 24-May-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/854,039

; FILING DATE: 09-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: MIV-079,04

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 197 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-865-018-4

Query Match 94.2%; Score 356; DB 10; Length 197;

Best local Similarity 92.5%; Pred. No. 2.9e-34;

Matches 62; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACNPLGPDVHEELTRDLKKHCRDMEASQRKWNFDQNHKPLEGKYEWQVEVK 60

|||||

Db 22 EYKPSACNPLGPDVHEELTRDLKKHCRDMEASQRKWNFDQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67

|||||

Db 82 GSLPEFY 88

## RESULT 11

US-08-902-572-26

; Sequence 26, Application US/08902572

; Patent No. US20020068706A1

; GENERAL INFORMATION:

; APPLICANT: Gyuris, Jeno

; APPLICANT: Lamphere, Lou

; APPLICANT: Beach, David H.

; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND

; TITLE OF INVENTION: RELATED THERETO

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/902,572

; FILING DATE: 29-JUL-1997

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: MIV-069,03

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 237 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-902-572-26

Query Match 93.7%; Score 354; DB 8; Length 237;

Best local Similarity 94.0%; Pred. No. 6.1e-34;

Matches 63; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EYKPSACNPLGPDVHEELTRDLKKHCRDMEASQRKWNFDQNHKPLEGKYEWQVEVK 60

|||||

Db 9 EYKPSACNPLGPDVHEELTRDLKKHCRDMEASQRKWNFDQNHKPLEGKYEWQVEVK 68

QY 61 GSLPEFY 67

|||||

Db 69 GSLPEFY 75

## RESULT 12

US-08-902-572-28

; Sequence 28, Application US/08902572

; Patent No. US20020068706A1

; GENERAL INFORMATION:

; APPLICANT: Gyuris, Jeno

; APPLICANT: Lamphere, Lou

; APPLICANT: Beach, David H.

; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND

; TITLE OF INVENTION: RELATED THERETO

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

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1  APPLICANT NUMBER: 05/06/02/0522
2  FILING DATE: 29 JUL 1997
3  CLASSIFICATION: 614
4  AUDREY/WEB: INFORMATION:
5  NAME: VINCENT, MATTHEW P.
6  REGISTRATION NUMBER: 00,100
7  REFERENCE NUMBER: 00,100
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: 617 832 7000
10 TELEFAX: 617 832 7000
11 INFORMATION FOR SEQ ID NO: 20:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 252 amino acids
14 TYPE: amino acid
15 SUBANALYSIS:
16 PHYSIOLOGY: THROST
17 MOLECULE TYPE: protein
18 DR 0602 072 28

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1  APPLICANT NUMBER: 05/06/02/0522
2  FILING DATE: 29 JUL 1997
3  CLASSIFICATION: 614
4  AUDREY/WEB: INFORMATION:
5  NAME: VINCENT, MATTHEW P.
6  REGISTRATION NUMBER: 00,100
7  REFERENCE NUMBER: 00,100
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: 617 832 7000
10 TELEFAX: 617 832 7000
11 INFORMATION FOR SEQ ID NO: 20:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 252 amino acids
14 TYPE: amino acid
15 SUBANALYSIS:
16 PHYSIOLOGY: THROST
17 MOLECULE TYPE: protein
18 DR 0602 072 28

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100 09 09 221 268 3

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Query Match 39.28, Score 148, DB 9, Length 164;  
Best Local Similarity 42.68, Pred. No. 6.5e-10;  
Matches 26, Conservative 12, Mismatches 24, Indels 0, Gaps 0,  
QY 7 ACNLEGEVNHHEITRIIEKERRTMEFFASGEKWNLEFQNHKPIFKYEWQVEVEKGSLLPEF 66  
DB 17 ACNLEGEVNDSPQISPDQDALMAGCIGAPRPWNNEDEVTETPLEGDFAWPVPVGLPKL 76  
QY 67 Y 67  
DB 77 Y 77

Search completed: May 30, 2003, 09:05:12  
Job time : 6.8385 secs



Genome version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 08:54:42 - Search time 5.6262 seconds  
(without alignments)  
1144.739 Million cell updates/sec

Title: US-09-865-018b-6\_copy\_22\_88

Perfect score: 378  
Sequence: 1 EYKPSACPNLFQVNHDEL PLFKYEWQVEKSLPEFY 67

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2050000000  
Post-Processing: Minimum Match 9%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR73:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	357	94.4	198	152718	gene p27kip1 prote
2	356	94.2	197	149064	cyclin-cdk inhibit
3	176	46.6	416	702424	cyclin-dependent k
4	172	45.5	210	151683	cyclin-dependent k
5	168	44.4	348	149262	cyclin-cdk inhibit
6	155	41.0	164	184725	tumor suppressor p
7	148	39.2	181	168674	cyclin-dependent k
8	146	38.6	181	154480	cyclin-dependent k
9	141	37.3	159	149023	tumor suppressor p
10	138	36.5	143	A49438	p53 tumor suppress
11	115.5	30.6	258	124499	hypothetical prote
12	108	26.5	191	781132	cyclin-dependent k
13	87.5	23.1	184	124496	hypothetical prote
14	74.5	19.7	470	250083	phosphatase - short
15	73.5	19.4	489	S63401	hypothetical prote
16	71.5	18.9	195	H96532	hypothetical prote
17	71.5	18.9	196	T09968	cyclin-dependent k
18	69.5	18.4	533	S52046	deoxyribodipyrimid
19	69	18.3	279	T26166	hypothetical prote
20	67.5	17.9	209	146149	hypothetical prote
21	67.5	17.9	246	149770	hypothetical prote
22	67	17.7	120	AB1425	hypothetical prote
23	66.5	17.6	171	T40598	hypothetical prote
24	66	17.5	327	T00797	hypothetical prote
25	65	17.2	317	770863	hypothetical prote
26	65	17.2	746	GC2838	enhancer of zeste
27	64.5	17.1	437	T28180	hypothetical prote
28	64.5	17.1	903	T20804	hypothetical prote
29	64	16.9	417	S51961	FUN50 protein ye

100 kDa coactivator  
sucrose synthase (hypothetical prote  
probable coiled coil  
chromosome scaffold  
translation initiation  
amino acid ABC transporter  
thymidylate synthase  
hypothetical prote  
centromere-binding  
chromosome segregator  
hypothetical prote  
S11 protein, self-phenylethanolamine  
probable lipoprotein  
alkaline phosphatase

ALIGNMENTS

RESULT 1

152718  
gene p27kip1 protein - human  
C:Species: Homo sapiens (man)  
C>Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000  
C:Accession: 152718  
R:Pietepol, J.A.; Bohlander, S.K.; Sato, Y.; Papadopoulos, N.; Liu, B.; Friedman, R.  
Cancer Res. 55, 1206-1210, 1995  
A:Title: Assignment of the human p27kip1 gene to 12p13 and its analysis in leukemias.  
A:Reference number: 152718; MUID:95188144; PMID:7882309  
A:Accession: 152718  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-198 <RES>  
A:Cross-references: GB:S76988; NID:3998402; PIDN:AA014244.1, PID:94261944  
C:Genetics:  
A:Gene: p27kip1  
A:Introns: 159/1

Query Match 94.4% Score 357; DB 2; Length 198;  
Best Local Similarity 94.0% Pred. No. 2.5e-32;  
Matches 63; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Q7 1 EYKPSACPNLFQVNHDELTKHRRDMEASQKKNFDFQNIKPLEGKYEWQVEK 60  
DB 22 DHPKPSACPNLFQVNHDELTKHRRDMEASQKKNFDFQNIKPLEGKYEWQVEK 81  
Q7 61 GSUPEFY 67  
DB 82 GSUPEFY 88

RESULT 2

149064  
cyclin, cdk inhibitor p27 - mouse  
N:Alternative names: cdk p27, G1 cyclin-cyclin-dependent kinase inhibitor p27  
C:Species: Mus musculus (house mouse)  
C>Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 05-Nov-1999  
C:Accession: 149064  
R:Toyoshima, H.; Hunter, T.  
Cell 78, 67-74, 1994  
A:Title: p27, a novel inhibitor of G1 cyclin-cdk protein kinase activity, is related  
A:Reference number: A54839; MUID:94366519; PMID:8033213  
A:Accession: 149064  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-197 <RES>  
A:Cross-references: EMBL:U10446; NID:3532771; PIDN:AAA21144.1, PID:3532772  
C:Keywords: cell cycle control

Query Match 94.2% Score 356; DB 2; Length 197;  
Best Local Similarity 92.5% Pred. No. 3.4e-32;





Hum. Mol. Genet. 4, 1029-1032, 1995  
 A:Title: Two variants of the Cipl/WAF1 gene occur together and are associated with human  
 A:Reference number: 154380; MUID:95384154; PMID:7655464  
 A:Accession: 168674  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-181 <RES>  
 R:Harper, J.W.; Adams, G.R.; Wei, N.; Keyomarsi, K.; Elledge, S.J.  
 Cell 75, 805-816, 1993  
 A:Title: The p21 cdk-interacting protein Cipl is a potent inhibitor of G1 cyclin-dependent  
 A:Reference number: A49437; MUID:94061996; PMID:8242751  
 A:Accession: A49437  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 18-181 <RES>  
 A:Cross-references: GB:147233; MUID:9298078; PIDN:AAH59559.1; PID:9986879  
 R:Noda, A.; Ning, Y.; Venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.  
 Exp. Cell Res. 211, 90-98, 1994  
 A:Title: Cloning of sequence cell-derived inhibitors of DNA synthesis using an express  
 A:Reference number: 153412; MUID:94170884; PMID:8125163  
 A:Accession: 153412  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 18-181 <RES>  
 A:Cross-references: GB:126165; MUID:9418817; PIDN:AAAL9811.1; PID:9433742  
 P:Xiong, Y.; Hancock, G.J.; Zhang, H.; Casse, D.; Kobayashi, F.; Beach, D.  
 Nature 366, 701-704, 1993  
 A:Title: p21 is a universal inhibitor of cyclin kinases  
 A:Reference number: S39357; MUID:94081955; PMID:8259214  
 A:Accession: S39357  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 18-181 <XIO>  
 A:Cross-references: GB:S67388; MUID:9453134; PIDN:AAH29246.1; PID:9453135  
 C:Genetics:  
 A:Gene: Cipl/WAF1

Query Match 39.2%; Score 148; DB 2; Length 181;  
 Best Local Similarity 42.6%; Pred. No. 3.8e-09;  
 Matches 26, Conservative 11, Mismatches 24, Indels 0, Gaps 0,

QY 7 ACRLLFGPVNHFFELTRLEKHFHFMEEASQPKNFDFQNHKPLEGKYEWQFVEKGSILPEF 56  
 DB 34 ACRLLFGPVNHFFELTRLEKHFHFMEEASQPKNFDFQNHKPLEGKYEWQFVEKGSILPEF 93  
 QY 67 Y 67  
 DB 94 Y 94

RESULT 8  
 154380  
 cyclin-dependent kinase - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Jul-1994 #sequence\_revision 02-Jul-1995 #text\_change 21-Jul-2000  
 C:Accession: 154380  
 R:Mousses, S.; Ozcelik, H.; Lee, P.D.; Malkin, D.; Ball, S.B.; Andriulis, T.L.  
 Hum. Mol. Genet. 4, 1049-1052, 1995  
 A:Title: Two variants of the Cipl/WAF1 gene occur together and are associated with human  
 A:Reference number: 154380; MUID:95384154; PMID:7655464  
 A:Accession: 154380  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-181 <RES>  
 A:Cross-references: GB:147232; MUID:9984723; PIDN:AAH59559.1; PID:9984724  
 C:Genetics:  
 A:Gene: Cipl/WAF1

Query Match 38.6%; Score 146; DB 2; Length 181;  
 Best Local Similarity 42.6%; Pred. No. 6.4e-09;  
 Matches 26, Conservative 10, Mismatches 25, Indels 0, Gaps 0;

QY 7 ACRLLFGPVNHFFELTRLEKHFHFMEEASQPKNFDFQNHKPLEGKYEWQFVEKGSILPEF 56  
 DB 34 ACRLLFGPVNHFFELTRLEKHFHFMEEASQPKNFDFQNHKPLEGKYEWQFVEKGSILPEF 93  
 QY 67 Y 67  
 DB 94 Y 94

RESULT 9  
 149023  
 tumor suppressor p21 WAF1/CIP1 [imported] - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Jun-2000  
 C:Accession: 149023; 149296  
 R:Suppl, K.; Siwarski, D.; Doslik, J.; Michl, P.; Chedid, M.; Reed, S.; Mock, B.; G.  
 Oncogene 9, 3017-3020, 1994  
 A:Title: Molecular cloning, sequencing, chromosomal localization and expression of mo  
 A:Reference number: 149023; MUID:94366761; PMID:8084607  
 A:Accession: 149023  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-159 <RES>  
 A:Cross-references: EMBL:U09507; MUID:9595302; PIDN:AAH60456.1; PID:9595303  
 R:El-Deiry, W.S.; Tokino, T.; Waldman, T.; Velculescu, V.; Lin, J.D.; Burrell, M.;  
 Cancer Res. 55, 2913-2919, 1995  
 A:Title: 1-q11-q14:clonal control of p21WAF1/CIP1 expression in normal and neoplastic tiss  
 A:Reference number: 149296; MUID:95316868; PMID:7796420  
 A:Accession: 149296  
 A>Status: nucleic acid sequence not shown, translation not shown, translated from GB/  
 A:Molecule type: mRNA  
 A:Residues: 1-159 <RES>  
 A:Cross-references: EMBL:U04174; MUID:9902578; PIDN:AAH52220.1; PID:9902579  
 C:Genetics:  
 A:Gene: Waf1

Query Match 37.3%; Score 141; DB 2; Length 159;  
 Best Local Similarity 39.1%; Pred. No. 2e-08;  
 Matches 25, Conservative 11, Mismatches 28, Indels 0, Gaps 0,

QY 4 KPSAFCNLGPGVNHFFELTRLEKHFHFMEEASQPKNFDFQNHKPLEGKYEWQFVEKGSIL 63  
 DB 13 KPSAFCNLGPGVNHFFELTRLEKHFHFMEEASQPKNFDFQNHKPLEGKYEWQFVEKGSIL 72  
 QY 64 PEY 67  
 DB 73 PKVY 76

RESULT 10  
 A49438  
 p53 tumor suppressor mediator WAF1 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 18-Nov-1994  
 C:Accession: A49438  
 R:El-Deiry, W.S.; Tokino, T.; Velculescu, V.E.; Levy, D.R.; Parsons, R.; Trent, J.M.;  
 Cell 75, 817-825, 1993  
 A:Title: WAF1, a potential mediator of p53 tumor suppression.  
 A:Reference number: A49438; MUID:94061997; PMID:8242752  
 A:Accession: A49438  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-143 <ELL>  
 A:Note: sequence extracted from NCI backbone (NCIN 140007, NCI-P140008)

Query Match 36.5%; Score 138; DB 2; Length 143;  
 Best Local Similarity 37.5%; Pred. No. 3.8e-08;  
 Matches 24, Conservative 13, Mismatches 27, Indels 0, Gaps 0;

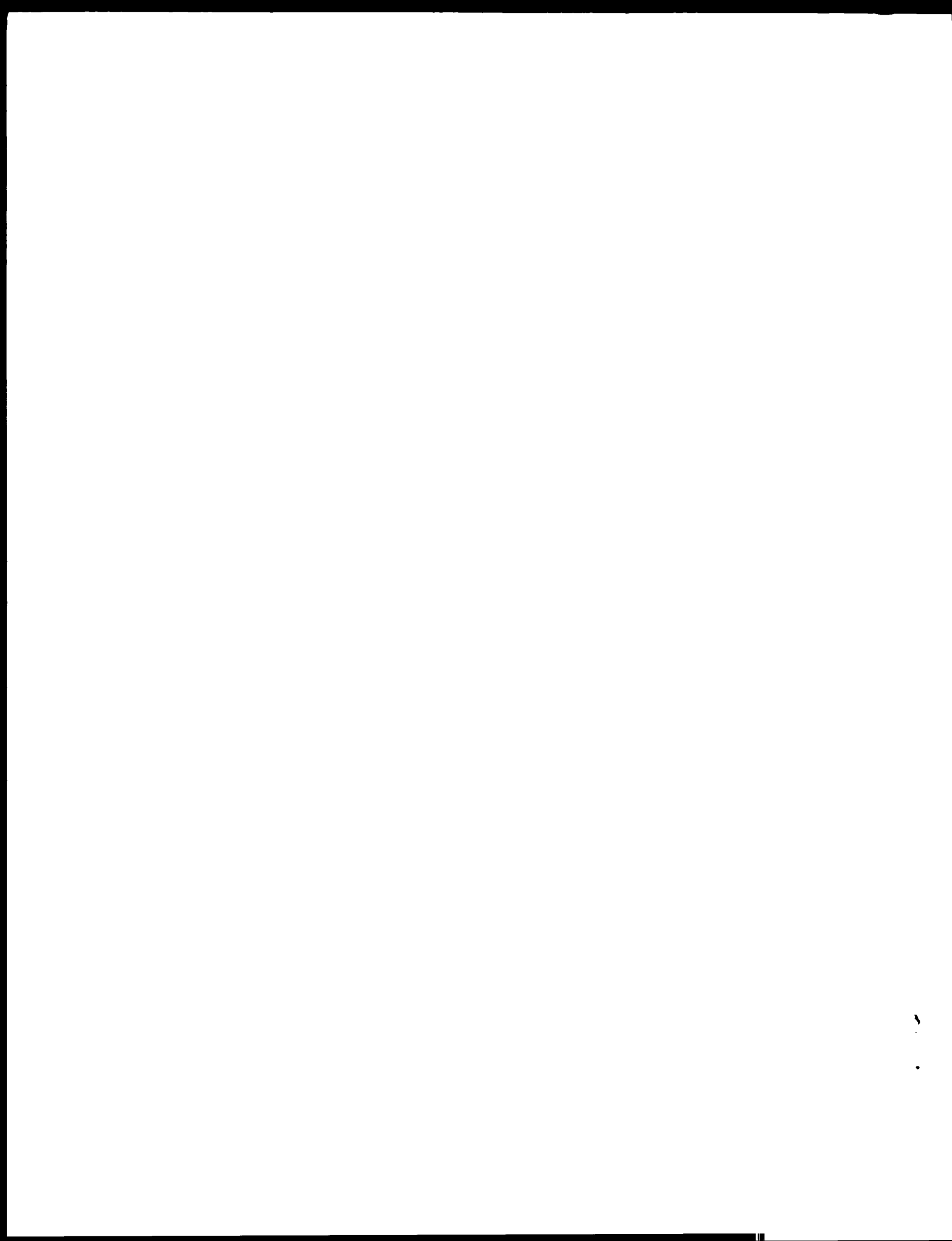
QY 4 KPSAFCNLGPGVNHFFELTRLEKHFHFMEEASQPKNFDFQNHKPLEGKYEWQFVEKGSIL 63  
 DB 13 KPSAFCNLGPGVNHFFELTRLEKHFHFMEEASQPKNFDFQNHKPLEGKYEWQFVEKGSIL 72



N:Alternate names: hypothetical protein N3555  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 19-Apr-2002  
 C:Accession: S63401  
 R:Dreescherboff, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.  
 submitted to the Protein Sequence Database, April 1996  
 A:Reference number: S62944  
 A:Accession: S63401  
 A:Molecule type: DNA  
 A:Residues: 1-489 <DUF>  
 A:Cross-references: EMBL:U77144; NID:gl002301; FID:0249869; PID:gl002602; USFDB:GN000014;  
 C:Experimental source: strain S288C  
 C:Genetics:  
 A:Gene: MIPS:YNR069c  
 A:Cross-references: SGD:S0005352  
 A:Map position: 14R

Query Match 19.4% Score 73.5; DB 2; Length 489;  
 Best Local Similarity 25.3%; Prod. NO. 2.3;  
 Matches 20; Conservative 10; Mismatches 14; Indels 35; Gaps 3;  
 QY 14 FVNHEELIKDLEK-----HRRDMEEASCKKWNEDFQNHKP 48  
 DB 413 PISREKCLKDIEDFDIEIANRLGMEIKYVFSKIERAIPHKEDIQEANRS-----DQLSP 466  
 QY 49 LEGKYEWQV-----EKSL 63  
 DB 467 LRGKYEWNAVAGNTENGTL 485

Search completed: May 30, 2003, 09:02:47  
 Job time : 6.62662 secs



GenCore version 5.1.6  
Copyright (c) 1993-2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:52:42, Search time: 0.8555 seconds  
(without alignments)  
972 808 Million full updates/sec

Title: US-09-865-018b-6\_copy\_22\_88  
Perfect score: 378  
Sequence: 1 EYKPSACNLEGFVNHEEL.....PLFGKYRWQVEKSLPEFY 67

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
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Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	100.0	178	1	CDNB_MUSVI
2	470	97.9	198	1	CDNB_FELCA
3	360	95.2	198	1	CDNB_HUMAN
4	356	94.2	197	1	CDNB_MOUSE
5	351	92.9	198	1	CDNB_CRICR
6	376	46.6	316	1	CDNC_HUMAN
7	168	44.4	348	1	CDNC_MOUSE
8	148	39.2	164	1	CDNL_HUMAN
9	144	38.1	164	1	CDNL_FELCA
10	141	37.3	159	1	CDNL_MOUSE
11	74.5	19.7	532	1	PHF_FOTTP
12	73.5	19.4	484	1	YNSR_YEAST
13	66.5	17.6	171	1	YSOL_CAEEL
14	65	17.2	1129	1	UBPC_GCHPO
15	64	16.9	417	1	YAC2_YEAST
16	63.5	16.8	808	1	SUS2_DAFCA
17	63	16.7	261	1	YC92_HAEIN
18	63	16.7	886	1	SXNE_HUMAN
19	63	16.7	899	1	YABD_SCHPO
20	62.5	16.5	611	1	IF4B_HUMAN
21	62	16.4	746	1	E2H2_HUMAN
22	61.5	16.3	125	1	PR32_DROME
23	61.5	16.3	956	1	CB31_YEAST
24	61	16.1	282	1	PRMT_HUMAN
25	61	16.1	584	1	ENV1_HUMAN
26	60.5	16.0	380	1	NTG2_YEAST
27	60.5	16.0	333	1	PCB2_HUMAN
28	60	15.9	612	1	DNAX_LISIN
29	60	15.9	517	1	PNAX_LISIN
30	60	15.9	751	1	Z184_HUMAN
31	60	15.9	1513	1	PPDQ_OPYSA
32	59.5	15.7	301	1	OMPG_ECOLI
33	59.5	15.7	358	1	ARCB_CORPS

34	59.5	15.7	570	1	HAG_NITEU
35	59.5	15.7	801	1	SUS2_DAFCA
36	59.5	15.7	157	1	IVA1_CVI
37	59	15.6	203	1	YD41_HAEIN
38	59	15.6	386	1	PNAL_SCHPO
39	59	15.6	486	1	CATA_RACFP
40	59	15.6	639	1	GLCX_SOYBN
41	59	15.6	670	1	KSPA_HVIN
42	59	15.6	670	1	KSPA_HUMAN
43	59	15.6	670	1	KSPA_HAFIT
44	59	15.6	686	1	KGPB_BOVIN
45	59	15.6	686	1	KGPB_HUMAN

ALIGNMENTS

RESULT 1	CDNB_MUSVI	STANDARD;	PRT;	178 AA.
AC	P46529;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase inhibitor p27) (p27Kip1) (Fragment).			
GN	CDKN1B.			
OS	Mustela vison (American mink).			
OC	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;			
OC	Mustela.			
UX	NCBITaxID=9667;			
FN	[1]			
RV	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=94306518; PubMed=8033212;			
RA	Polyak K, Lee M-H, Friedman-Hromage H, Koff A, Roberts JM,			
RA	Tempest P, Massague J;			
RI	"Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a potential mediator of extracellular antimitogenic signals.";			
RT	Cell 78:59-66(1994).			
PL	[2]			
FP	FUNCTION.			
EX	MEDLINE=94116862; PubMed=8288131;			
FA	Polyak K, Katu T-Y, Solomon M J, Sherr CJ, Massague J,			
FA	Roberts J.M., Koff A.;			
RT	"p27Kip1, a cyclin-Cdk inhibitor, links transforming growth factor-beta and contact inhibition to cell cycle arrest ";			
PL	Genes Dev 8:9-22(1994).			
CC	-1- FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1 arrest. Binds to and inhibits complexes formed by cyclin E/Cdk2, cyclin A/Cdk2, and cyclin B1/Cdk4. Interaction with nucleoprotein NP50 is required for nuclear import and for degradation of phosphorylated p27Kip1 after nuclear import. (By similarity)			
CC	-1- SUBUNIT: Interacts with NP50 (by similarity).			
CC	-1- SUBCELLULAR LOCATION: Nuclear			
CC	-1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.			
CC	-----			
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CC	-----			
DR	EMBL: U00004. AAA0234.1.			
DR	InterPro: IPR003175; CDI.			
DR	Tram: PF02234, CDI, 1.			
KW	Cell cycle; Nuclear protein.			
FT	DOMAIN 153 169 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).			
FT	NON_TER 178 178			
SEQUENCE	178 AA: 20129 MW: 1051044010473E CRC64;			

[illegible]

AC011	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85																

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DR EMBL: AF480891; AAL78041.1; -
DR PDB: 1JUS; 29-JUL-97; -
DR SWISS-2DPAGE: P46527; HUMAN.
DR GenBank: U09988; 1785; CHIKV
DR MIM: 600778; -
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
DR Cell cycle; Nuclear protein; 3D-structure; Polymorphism.
KW DOMAIN 153 169 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
FT VARIANT 15 15 R->W (IN DBSNP:2066827).
FT VARIANT 109 109 V->G (IN DBSNP:2066827).
FT CONFLICT 22 22 E>D (IN REF. 2).
FT SEQUENCE 198 AA: 22073 MW: 1118056901; (F343) Q6064;
SQ
Query Match 95.2%; Score 360; DB 1; Length 198;
Best Local Similarity 95.5%; Pred. No. 1 9e-32;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EYKPSACNLFQGVNHEELTPNFKHKIMEASQKWNFFQNHKPLESKYEWQVEVK 60
DB 22 EHPKPSACNLFQGVNHEELTPNFKHKIMEASQKWNFFQNHKPLESKYEWQVEVK 81
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88
RESULT 4
CNDB_MOUSE
ID CNDB_MOUSE STANDARD; PRT; 197 AA.
AC P46414;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cyclin dependent kinase inhibitor 1B (Cyclin-dependent kinase
DE Inhibitor p27) (p27Kip1).
GN CDKN1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
FX MEDLINE=94306519; PubMed=833212;
RA Toyoshima H., Hunter T.,
RT "p27, a novel inhibitor of G1 cyclin-Cdk protein kinase activity, is
RT related to p21".
RL Cell 78:67-74(1994).
RN [2]
RP SEQUENCE FROM N.A.
FX MEDLINE=94306518; PubMed=833212;
RA Polyak K., Lee M.-H., Eddington-Bromage H., Koff A., Roberts J.M.,
RA Tempest P., Massague J.,
RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a
RT potential mediator of extracellular antimitogenic signals".
RL Cell 78:59-66(1994).
RN [3]
RP INTERACTION WITH NUP50, AND MUTAGENESIS.
RC STRAIN=RALB/C;
RX MEDLINE=20271857; PubMed=10811608;
RA Mueller D., Thiele K., Huerquin A., Diekmann A., Eilers M.;
RT "Cyclin E-mediated elimination of p27 requires its interaction with
RT the nuclear pore-associated protein MNPAP50".
PL EMBO J. 19:2168-2180(2000).
CC
CC -!- FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1
CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,
CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin
CC NUP50 is required for nuclear import and for degradation of
CC phosphorylated p27Kip1 after nuclear import (By similarity).
CC -!- SUBUNIT: Interacts with NUP50 (By similarity).
CC -!- SURCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
CC
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RX MEDLINE-95247028; PubMed-7729664;  
RA Matsuo S., Edwards M.C., Bai C., Parker S., Zhang P., Baldini A.,  
RA Harper J.W., Elledge S.J.;  
RT "p57KIP2, a structurally distinct member of the p21CIP1 Cdk inhibitor  
RT family, is a candidate tumor suppressor gene."  
RL Genes Dev. 9:650-662(1995).  
CC -1- FUNCTION: POTENT TIGHT-BINDING INHIBITOR OF SEVERAL G1 CYCLIN/CDK  
CC COMPLEXES (CYCLIN E-CDK2, CYCLIN D2-CDK4, AND CYCLIN A-CDK2) AND,  
CC TO LESSER EXTENT, OF THE MITOTIC CYCLIN B-CDK2. NEGATIVE REGULATOR  
CC OF CELL PROLIFERATION. MAY PLAY A ROLE IN MAINTENANCE OF THE  
CC NONPROLIFERATIVE STATE THROUGHOUT LIFE.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- TISSUE SPECIFICITY: IT IS EXPRESSED IN THE HEART, BRAIN, LUNG,  
CC SKELETAL MUSCLE, KIDNEY, PANCREAS AND TESTIS. HIGH LEVELS ARE SEEN  
CC IN THE PLACENTA WHILE LOW LEVELS ARE SEEN IN THE LIVER.  
CC -----  
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CC -----  
DR EMBL: U20553; AAC52186.1; -  
DR EMBL: U22399; AAAB5096.1; -  
DR MGI: MGI:104564; Cdkic.  
DR InterPro: IPR003175; Cdk.  
DR Pfam: PF02234; Cdk1; 1.  
KW Cell cycle; Alternative splicing  
FT DOMAIN 108 189 PRO-RICH.  
FT DOMAIN 178 284 GLU/ASP RICH  
FT DOMAIN 309 312 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)  
FT VARSPPLIC 1 13 MISSING (IN ISOFORM KIP2H/P57B).  
FT CONFLICT 150 151 DA -> EP (IN REF. 2).  
SQ SEQUENCE 348 AA; 37331 MW; 10BA85381D77016D4 Cw64;  
Query Match 44.4%; Score 168; DB 1; Length 348;  
Best Local Similarity 45.5%; Pred. No. 3.4e-11;  
Matches 30; Conservative 13; Mismatches 21; Indels 2; Gaps 1;  
QY 4 KPSACIFGPNVHEELTDLKHPDMEFASQPKWNEFQNHKPLE--GKYWEVEKRG 61  
Db 28 KSACIFGPNVHEELTDLKHPDMEFASQPKWNEFQNHKPLE--GKYWEVEKRG 61  
QY 62 SLPEFY 67  
Db 88 SVPAFY 93  
RESULT 8  
CDN1\_HUMAN STANDARD; PRT; 164 AA.  
AC P38936; Q9B0T4;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cyclin dependent kinase inhibitor 1 (p21) (CDK interacting protein 1)  
DE (Melanoma differentiation-associated protein 6) (MDA-6).  
GN CDKN1A or CDKN1 or CIP1 or WAF1 or MDA6 or SDI1 or P21 or CAP20.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID:9606;  
[1]  
CC SEQUENCE FROM N.A.  
RX MEDLINE-94061996; PubMed-8242751;  
RA Harper J.W., Adami G.R., Wei N., Koyama S.J.;  
RT "The p21 Cdk interacting protein Cipl is a potent inhibitor of G1  
RT cyclin-dependent kinases."  
RL Cell 75:805-816(1993)  
RN [2]  
CC SEQUENCE FROM N.A.

FX MEDLINE-94061997; PubMed-8242752;  
RA El-Deiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons P.,  
RA Trent J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.;  
RT "WAF1, a potential mediator of p53 tumor suppression."  
RL Cell 75:817-825(1993).  
RN [3]  
CC SEQUENCE FROM N.A.  
RX MEDLINE-94061955; PubMed-8254214;  
RA Xiong Y., Hannon G.J., Zhang H., Casso D., Kobayashi R., Beach D.;  
RT "p21 is a universal inhibitor of cyclin kinases."  
PL Nature 366:701-704(1993).  
RN [4]  
CC SEQUENCE FROM N.A.  
RA Jiang H., Fisher P.B.;  
RT "Use of a sensitive and efficient subtraction hybridization protocol  
RT for the identification of genes differentially regulated during the  
RT induction of differentiation in human melanoma cells."  
PL Mol. Cell. Differ. 1:285-294(1994).  
RN [5]  
CC SEQUENCE FROM N.A.  
RA Jiang H., Lin T., Herlyn M., Kerbel P.S., Weissman B.E.,  
RA Welch D.P., Fisher P.B.;  
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.  
RN [6]  
CC SEQUENCE FROM N.A.  
RX MEDLINE-94170884; PubMed-8125163;  
RA Noda A., Ning Y., Venable S.F., Pereira-Smith O.M., Smith J.R.;  
RT "Cloning of senescent cell-derived inhibitors of DNA synthesis using  
RT an expression screen."  
PL Exp. Cell Res. 211:90-98(1994).  
RN [7]  
CC SEQUENCE FROM N.A.  
RX MEDLINE-95384154; PubMed-7655464;  
RA Mousses S., Oezcelik H., Lee P.D., Malkin D., Pull S.R.,  
RA Andralis I.L.;  
RT "Two variants of the CIP1/WAF1 gene occur together and are associated  
RT with human cancer."  
PL Hum. Mol. Genet. 4:1089-1092(1995).  
RN [8]  
CC SEQUENCE FROM N.A., AND VARIANT ARG-31.  
RA Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,  
RA Nguyen D.A., Livingston P.T., Pool C.L., Robertson P.D.,  
RA Schackwitz W.S., Sherwood J.K., Wittrik L.A., Nickerson N.A.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN [9]  
CC SEQUENCE FROM N.A.  
RA Palmer S.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
RN [10]  
CC SEQUENCE FROM N.A., AND VARIANT ARG-31  
RA Straussberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [11]  
CC X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 139-160  
RX MEDLINE-97015085; PubMed-8861913;  
RA Curtis J.M., Kelman Z., Horwitz T., O'Donnell M., Kuriyan J.;  
RT "Structure of the C-terminal region of p21(WAF1/CIP1) complexed with  
RT human PCNA."  
RL Cell 87:297-306(1996).  
CC -1- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES  
CC ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO  
CC DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE  
CC ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT  
CC KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN ALL ADULT HUMAN TISSUES,  
CC WITH 5-10x HIGHER LEVELS OBSERVED IN THE BRAIN.  
CC -1- INDUCTION: BY P53, MYEUREIN (ANTITUMORIC COMPOUND) AND INTERFERON  
CC BETA.  
CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.  
CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;  
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/CDKN1AID139.html".



Cell 75:817-825(1993).

CC -1- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES  
CC ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO  
CC DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE  
CC ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT  
CC KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- INDUCTION: BY P53, MEZEREIN (ANTI-NEKEMIC COMPOUND) AND INTERFERON  
CC BETA.

CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.

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CC EMBL: U09507; AAC6456.1; .

CC EMBL: U24173; AAC52230.1; .

CC PIR: A49438; A49438.

CC MG: MG1:104556; Gdala.

CC InterPro: IPR003175; CD1.

CC Pfam: PF02234; CD1; .

CC Cell cycle: Nuclear protein; Zinc-finger.

CC ZNF-finger 12 43 C4-TYPE (POTENTIAL).

CC CONFLICT 30 30 P -> S (IN REF. 3).

CC CONFLICT 56 57 TP -> RQ (IN REF. 3).

CC SEQUENCE 159 AA: 17785 MW: 3787C22B9A2F5089 CRC64;

Query Match

Best Local Similarity 37.3%; Score 141; DB 1; Length 159;

Matches 25; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 4 KPSACHNLPVNHHELTPTDLEKHPWNEFASQPKWNFQNHKPKLECKYEWQEKSL 63

DB 13 RSKVCEIFSPVESELELPKCHALMAGSLYEAFERWNFDFVETPLEGFWVERKSL 72

QY 64 PEY 67

DB 73 PKVY 76

RESULT 11

PHR\_POTR

ID PHR\_POTR STANDARD: PRT: 532 AA.

AC Q28811;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Deoxyribodipyrimidine photolyase (6' 4' 1' 9' 3') (DNA photolyase)

DE (Photoreactivating enzyme).

OS Porcine tridactylus (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Diprotodontia; Macroplacidae; Peromys-

OC NCBI\_TaxID=9310;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE:95112925; PubMed:7813451;

FA Yasui A., Eker A.F., Yasui H., Kikuchi S., Takao M.,

RA Oikawa A.

RT "A new class of DNA photolyases present in various organisms including

RT apical mammals."

RL EMBL J. 13:6143-6151(1994).

CC -1- FUNCTION: THIS ENZYME CATALYZES THE LIGHT-DEPENDENT MONOMERIZATION

CC (300-600 NM) OF CYCLOHUIYL PYRIMIDINE DIMERS (IN CIS-SYN

CC CONFIGURATION), WHICH ARE FORMED BETWEEN ADJACENT BASES ON THE

CC SAME DNA STRAND, UPON EXPOSURE TO ULTRAVIOLET RADIATION.

CC -1- CATALYTIC ACTIVITY: Cyclobutadipyrimidine (in DNA) + 2 pyrimidine

CC residues (in DNA).

CC -1- COFACTOR: FAD.

CC -1- SIMILARITY: BELONGS TO THE DNA PHOTOLYASE CLASS-2 FAMILY.

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CC EMBL: U24020; HAA05041.1; .

CC InterPro: IPR000474; DNA\_photolyase.

CC InterPro: IPR000288; DNA\_photolyase\_2.

CC InterPro: IPR005101; FAD\_binding\_7.

CC Pfam: PF00875; DNA\_photolyase; 1.

CC Pfam: PF03441; FAD\_binding\_7; 1.

CC ProDom: PD007711; DNA\_photolyase\_2; 1.

CC TIGRFAMs: TIGR00591; phr2; 1.

CC PROSITE: PS01083; DNA\_PHOTOLYASES\_2; 1.

CC PROSITE: PS01084; DNA\_PHOTOLYASES\_2; 1.

CC KW Lyase, Chromophore; Flavoprotein; FAD; DNA repair; DNA-binding.

CC SEQUENCE 542 AA: 6163 MW: 68058186UE/BB4258 CPC64;

Query Match 19.7%; Score 74.5; DB 1; Length 532;

Best Local Similarity 29.5%; Pred. No. 0.9; Mismatches 28; Indels 23; Gaps 5;

Matches 26; Conservative 11; Mismatches 28; Indels 23; Gaps 5;

QY 3 PKPSACHN;-----F;PVNHHELTPTDLEKHPWNEFASQPKWNFQNHKPKLECKYEWQEKSL 44

DB 325 PNKIALSNLSWPFHFGQVSVQPAITLVQKHPSYPDSVTFNFEAVVPPPLADNFCYNK 384

QY 45 NHKPLECKYEWQEV-----EKGSLPEPY 67

DB 385 NYDKLEGAYDWAQTTTLRHAKDKRPHLY 412

RESULT 12

YN98\_YEAST

ID YN98\_YEAST STANDARD: PRT: 489 AA.

AC P53755;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Hypothetical 54.8 kDa protein in BIO3-HXT17 intergenic region.

GN YNR069C OR N3555.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,

RA Hilbert H., Muesli D.,

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO THE N-TERMINAL OF YEAST BUL1 AND YML111W.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: Z71684; CAA96351.1; .

CC SGD: S0005352; YNR069C.

CC KW Hypothetical protein.

CC SEQUENCE 489 AA: 54831 MW: 10657895F1CAPR34 CPC64;

Query Match 19.4%; Score 73.5; DB 1; Length 489;

Best Local Similarity 25.3%; Pred. No. 1.1; Mismatches 14; Indels 35; Gaps 3;

Matches 20; Conservative 10; Mismatches 14; Indels 35; Gaps 3;

QY 14 PVNHHELTDRLEK-----HRPDEEASQKWNFDQNHKP 48



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RESULT 15
YAG1_YEAST
ID YAG1_YEAST STANDARD; PRT; 417 AA.
AC P39713;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1
DE intergenic region.
GN YAL061W OR FUN50.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID:4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288c / AB972;
KX MEDLINE=95249563; PubMed=7731988;
RA Hussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
RA Hall J., Guelliette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
RA Storms K.K.;
RT "The nucleotide sequence of chromosome I from Saccharomyces
RT cerevisiae."
RL Proc. Natl. Acad. Sci. U S A 92:1809-1813(1995).
CC -|- COFACTOR: ZINC (Potential).
CC -|- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY.
CC -----
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CC -----
DR EMBL: U12480; AAC04973.1; -.
DR SGD: S0000057; YAL061W.
DR InterPro: IPR002328; ADH_zinc.
DR InterPro: IPR002085; Adh_zn_family.
DR Pfam: PF00107; adh_zinc; 1.
DR PROSITE: PS00059; ADH_ZINC; 1.
DR PROSITE: PS00059; ADH_ZINC; 1.
KW Hypothetical protein; Oxidoreductase; Zinc.
FT METAL 39 39 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 64 64 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 120 120 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 123 123 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 131 131 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 173 173 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 417 AA; 46098 MW; D921FDFRFAID00151 CPC54;
Query Match 16.9%; Score 64; DB 1; Length 417;
Best local similarity 34.3%; Pred No. 9.5;
Matches 12; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
QY 4 KPSACRNLFQPVNHEELTRDLEKRRHMEASQKK 38
Db | | | | | | | | | | | | | | | |
366 KESTIKITLTPNNHCELNREADNEKKFISLSSPK 400

```

Search completed: May 30, 2003, 08:59:13  
Job time : 3.85659 secs



GenCode version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 08:53:57 : Search time 11.686 Seconds  
(without alignments)  
1181.337 Million cell updates/sec

Title: US-09-865-018b-6\_copy\_22\_88

Perfect score: 478  
Sequence: 1 EYKPSACNRLFGPVNHEEL.....PLEGKYEWQVEVKGSLPEFY 67

Scoring table: RIGSIM62  
Gapop 10 0 0 Gapext 0 5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 206000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_21:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_protist:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_virus:\*
  - 16: sp\_bacteriaph:\*
  - 17: sp\_archaeap:\*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	97.9	172	6 Q9BEA5	Q9BEA5 sus scrofa
2	370	97.9	198	6 Q9BDC3	Q9BDC3 sus scrofa
3	360	95.2	158	4 Q43806	Q43806 homo sapien
4	360	95.2	198	4 Q9NYG6	Q9NYG6 homo sapien
5	360	95.2	198	4 Q9RNS6	Q9RNS6 homo sapien
6	359	95.0	197	11 Q08769	Q08769 rattus norv
7	359	95.0	197	11 Q35792	Q35792 rattus norv
8	357	94.4	184	4 Q9B100	Q9B100 homo sapien
9	218.5	57.8	179	13 Q9QYX4	Q9QYX4 brachydanio
10	172	45.5	210	13 Q91603	Q91603 xenopus lae
11	169	44.7	209	13 Q91646	Q91646 xenopus lae
12	168	44.4	335	11 Q91V06	Q91V06 mus musculu
13	155	41.0	164	11 Q64315	Q64315 rattus norv
14	148	39.2	164	4 Q961F1	Q961F1 homo sapien
15	146	38.6	181	4 Q14010	Q14010 homo sapien
16	115.5	30.6	258	5 Q22198	Q22198 caenorhabdi

ALIGNMENTS

RESULT 1

Q9BEA5 Q9BEA5 PRELIMINARY; PRT; 172 AA.  
AC Q9BEA5;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE P27K1pl degradation-resistant isoform (Fragment).  
GN P27K1PLR.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina, Suidae, Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
EX MEDLINE=21063196; PubMed=11115598;  
FA Hirano K., Hirano M., Zeng Y., Nishimura J., Hara K., Muta K.,  
RA Nawata H., Kanaide H.;  
RT "Cloning and functional expression of a degradation-resistant novel  
RI isoform of p27K1pl.";  
RL Biochem J 353:51-57(2001).  
DR EMEL; ARO41958; BAB39728.1; -.  
DR InterPro: IPR002047; AKH.  
DR Pfam: PF02234; CDI; 1.  
DR PPSITE: PS00256; AKH; UNKNOWN\_1.  
FT NON\_TER 1 1  
SQ SEQUENCE 172 AA; 10348 MW; 98FE2FAC8RC4A46E CPC64;

Query Match: 97.9%, Score 370, Lb 6, Length 172.  
Best local similarity 98.5%, Pred No. 17e-33,  
Matches 66; Conservative 0, Mismatches 1; Indels 0, Gaps 0.

Qy 1 EYKPSACNRLFGPVNHEELTLELKHPPHMEASQPKWNFDQNHKPLEGKYEWQVEVK 60  
Db 14 EYKPSACNRLFGPVNHEELTLELKHPPHMEASQPKWNFDQNHKPLEGKYEWQVEVK 73  
Qy 61 GSLPEFY 67  
|||||

Q9u5r5 caenorhabdi  
Q04154 arabidopsi  
Q8u809 arabidopsi  
Q8wqg2 drosophila  
Q22197 caenorhabdi  
Q94536 drosophila  
P91654 drosophila  
Q93v92 nicotiana t  
P91668 drosophila  
Q91j15 arabidopsi  
Q9fs28 pisum sativ  
Q9fk65 arabidopsi  
Q93yf6 nicotiana s  
Q9lr70 arabidopsi  
Q94cm0 arabidopsi  
Q48446 arabidopsi  
Q28464 monodelphis  
Q77670 canis fami  
Q9vr60 drosophila  
Q9fx90 arabidopsi  
Q94cl9 arabidopsi  
Q48597 chenopodiu  
Q9yuz9 human immu  
Q9er42 mus musculu  
Q23168 caenorhabdi  
Q8sf08 oryza sativ  
Q9scr2 arabidopsi  
Q03973 saccharomyc  
Q9h0g4 homo sapien





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Query Match          95.2%; Score 360; DB 4; Length 198;
Best Local Similarity 95.5%; Pred. No. 2.6e-32;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACNLPFGPVNHELTPOLEKHPDMEASQKWNFDQNHKPLESKYEWQVEVK 60
   1:|||||
Db 22 EHPKPSACNLPFGPVNHELTPOLEKHPDMEASQKWNFDQNHKPLESKYEWQVEVK 81
   1:|||||

QY 61 GSLPEFY 67
   1:|||||
Db 82 GSLPEFY 88
   1:|||||

RESULT 6
008769 PRELIMINARY; PRT; 197 AA.
AC 008769;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE P27 K1P1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawada M., Yamagoe S., Uehara Y.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kawada M., Yamagoe S., Kazuo S., Mizuno S., Uehara Y.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kawada M., Yamagoe S., Murakami Y., Suzuki K., Mizuno S., Uehara Y.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Dastvan F., Peidy M.A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; D86924; BAA19460.1; -;
DR EMBL; AF015194; AAB71368.1; -;
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
SQ SEQUENCE 197 AA; 22139 MW; 55738078C2D555B2 CRC64;

Query Match          95.0%; Score 359; DB 11; Length 197;
Best Local Similarity 94.0%; Pred. No. 3.3e-32;
Matches 63; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACNLPFGPVNHELTPOLEKHPDMEASQKWNFDQNHKPLESKYEWQVEVK 60
   1:|||||
Db 22 EHPKPSACNLPFGPVNHELTPOLEKHPDMEASQKWNFDQNHKPLESKYEWQVEVK 81
   1:|||||

QY 61 GSLPEFY 67
   1:|||||
Db 82 GSLPEFY 88
   1:|||||

RESULT 7
015792 PRELIMINARY; PRT; 197 AA.
AC 015792;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE P27.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=SPLEEN;
PX MFTLINE=97361761; PubMed=9218722;
PA Nomura H., Sawada Y., Fujinaga K., Ohtaki S.;
PT "Cloning and characterization of rat p27Kip1, a cyclin-dependent
   kinase inhibitor.";
RL Gene 191:211-218(1997).
DR EMBL; D83792; BAA21561.1; -;
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
SQ SEQUENCE 197 AA; 22112 MW; 55738078C2D555B2 CRC64;

Query Match          95.0%; Score 359; DB 11; Length 197;
Best Local Similarity 94.0%; Pred. No. 3.3e-32;
Matches 63; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACNLPFGPVNHELTPOLEKHPDMEASQKWNFDQNHKPLESKYEWQVEVK 60
   1:|||||
Db 22 EHPKPSACNLPFGPVNHELTPOLEKHPDMEASQKWNFDQNHKPLESKYEWQVEVK 81
   1:|||||

QY 61 GSLPEFY 67
   1:|||||
Db 82 GSLPEFY 88
   1:|||||

RESULT 8
096TE0 PRELIMINARY; PRT; 198 AA
AC 096TE0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Cdk inhibitor p27Kip1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MDLINE=2937222; PubMed=10913178;
RA Millard S.S., Vidal A., Markus M., Koff A.;
RT "A Urlich element in the 5' untranslated region is necessary for the
   RT translation of p27 mRNA.";
RL Mol. Cell. Biol. 20:5947-5959(2000).
DR EMBL; AY042555; AAF88142.1; -;
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
SQ SEQUENCE 198 AA; 22017 MW; 81F8F338AA00248 CRC64;

Query Match          94.4%; Score 357; DB 4; Length 198;
Best Local Similarity 94.0%; Pred. No. 5.5e-32;
Matches 63; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACNLPFGPVNHELTPOLEKHPDMEASQKWNFDQNHKPLESKYEWQVEVK 60
   1:|||||
Db 22 EHPKPSACNLPFGPVNHELTPOLEKHPDMEASQKWNFDQNHKPLESKYEWQVEVK 81
   1:|||||

QY 61 GSLPEFY 67
   1:|||||
Db 82 GSLPEFY 88
   1:|||||

RESULT 9
090YX4 PRELIMINARY; PRT; 179 AA.
AC 090YX4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE p27-like cyclin-dependent kinase inhibitor.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RN  [4]
RP  SEQUENCE FROM N.A.
RC  SPECIES=Mouse; TISSUE=BREAST TUMOR;
RA  Scrausberg K.;
RL  Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR  EMRL: A1276505; CAC16402.1; -.
DF  EMBL: AF160190; AAF00683.1; -.
DR  EMBL: BC005412; AAE05412.1; -.
DF  MGD: MGI-104564; Cdkn1c.
DR  InterPro: IPR003175; CDI.
DR  Pfam: PF02234; CDI, 1.
KW  Kinase.
SQ  SEQUENCE 335 AA; 35903 MW; E5C40675287FEB3F CRC64;

  Query Match 44.4%; Score 168; DB 11; Length 335;
  Best Local Similarity 45.5%; Pred. No. 1.2e-09;
  Matches 30; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

QY  4 KPSACNLFGPVNHEELTRDLEKHKRDMEEASQKWNFDQNHKPLEGKYEWQVEKGS 61
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  15 RSSACRSIFGVPVHFEIISPELMPRTAFINAFINQNDNFQDQVPLRGKQLQWNEVDSE 74
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  62 SLPEFY 67
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  75 SVPAFY 80
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
Q64315
ID  Q64315 PRELIMINARY; PPT; 164 AA.
AC  Q64315;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  P21 (WAF1).
GN  WAF1 OR CIP1.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  MEDLINE=9531644; PubMed=7706420;
RX  Belinsky S.A.;
RL  Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR  EMBL: U24174; AAC52231.1; -.
DR  EMBL: U41275; AAC42084.1; -.
DR  InterPro: IPR003175; CDI.
DR  Pfam: PF02234; CDI, 1.
SQ  SEQUENCE 164 AA; 18418 MW; 6057F86604586435F CRC64;

  Query Match 41.0%; Score 155; DB 11; Length 164;
  Best Local Similarity 40.6%; Pred. No. 1.2e-09;
  Matches 26; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY  4 KPSACNLFGPVNHEELTRDLEKHKRDMEEASQKWNFDQNHKPLEGKYEWQVEKGS 63
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  13 RSKVGRPLFGPVDSQSLSPDQDALMASQIQEAPERNFDFATETPLEGNYWYWRSPCL 72
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  64 PEFY 67
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  73 PKIY 76
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 14
Q96LE1
ID  Q96LE1 PRELIMINARY; PPT; 164 AA.
AC  Q96LE1;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Cyclin dependent kinase inhibitor isoform.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  Li L.-C.; Zhao H.; Dahiya R.;
RC  "Cloning and Characterization of p21 Isoform.";
RL  Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AY008263; AAG15411.1; -.
DR  InterPro: IPR003175; CDI.
DR  Pfam: PF02234; CDI, 1.
KW  Kinase.
SQ  SEQUENCE 164 AA; 17827 MW; 378E002161FB3BD7 CRC64;

  Query Match 39.2%; Score 148; DB 4; Length 164;
  Best Local Similarity 42.6%; Pred. No. 7.5e-09;
  Matches 26; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY  7 ACRLFGPVNHEELTRDLEKHKRDMEEASQKWNFDQNHKPLEGKYEWQVEKGS 66
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  67 Y 67
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  77 Y 77
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
Q14010
ID  Q14010 PRELIMINARY; PPT; 181 AA.
AC  Q14010;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Cyclin-dependent kinase (Fragment).
GN  CIP1/WAF1.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=TUMOR;
RX  MEDLINE=95384154; PubMed=7655464;
RA  Mousses S.; Ozcelik H.; Lee P.D.; Malkin D.; Bull S.B.; Andrulis I.L.;
RT  "Two variants of the CIP1/WAF1 gene occur together and are associated
RT  with human cancer.";
RL  Hum. Mol. Genet. 4:1089-1092(1995).
DR  EMBL: L47232; AAB59559.1; -.
DR  InterPro: IPR003175; CDI.
DR  Pfam: PF02234; CDI, 1.
KW  Kinase.
FT  NON_TER
SQ  SEQUENCE 181 AA; 20083 MW; 4CCFA5112232D4F1 CRC64;

  Query Match 38.6%; Score 146; DB 4; Length 181;
  Best Local Similarity 42.6%; Pred. No. 1.4e-08;
  Matches 26; Conservative 10; Mismatches 25; Indels 0; Gaps 0;

QY  7 ACRLFGPVNHEELTRDLEKHKRDMEEASQKWNFDQNHKPLEGKYEWQVEKGS 66
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  34 ACRLFGPVDSQSLSPDQDALMAGCIQEARERNFDFVETPLEGDFAWERVRLGLPKL 93
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  67 Y 67
Db  : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Search completed: May 30, 2004, 09:01:44  
Job time : 12.686 secs